

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number 116579

TO: Rita Mitra

Location: REM-3B65

Art Unit: 1653

Monday, March 15, 2004

Case Serial Number: 09/976740

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

#### Search Notes

Dear Examiner Mitra,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 

took for World. I Pot. here.





# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 116472

TO: Rita Mitra

Location: REM/3B65

**Art Unit: 1653** 

Monday, March 15, 2004

Case Serial Number: (09/976740

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen E01A69

Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

RUSH

Search and Information Resources Administration

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Result
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q-/Ggp2_1/USPTO_spool_p/US09975740/runat_10032004_094549_19588/app_query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-bitsoun62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09976740_@CGN 1 1 712 @runat 10032004_094549 19588
-NCFU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGS_GCORES=0 -WAIT_-DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein - nucleic search, using frame_plus_p2n model
                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length:
seq length:
                                                                                                                      Published Applications_NA:*

1: /cgm2_6/ptcdata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgm2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgm2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgm2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgm2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgm2_6/ptcdata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgm2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgm2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

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10: /cgm2_6/ptcdata/1/pubpna/US09A_PUBCOMB.seq:*

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12: /cgm2_6/ptcdata/1/pubpna/US09B_PUBCOMB.seq:*

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15: /cgm2_6/ptcdata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgm2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgm2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgm2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*

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16: /cgm2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgm2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgm2_6/ptcdata/1/pubpna/US10B_PUB.seq:*
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Query
Match Length DB
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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Copyright (c) 1993 - 2004 Compugen Ltd
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  Description
                                                                                                                                                                                                              RESULT 1
US-09-962-055-31
Sequence 31, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                      STATE: MA
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Law, Simon W.
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136 100.0 78 9 US-09-062-055-31 Sequence 31, Appl 136 100.0 78 12 US-10-971-742-31 Sequence 31, Appl 136 100.0 78 13 US-10-071-742-31 Sequence 31, Appl 136 100.0 78 13 US-10-072-523-31 Sequence 31, Appl 136 100.0 78 13 US-10-072-523-31 Sequence 31, Appl 136 100.0 78 13 US-10-072-523-31 Sequence 31, Appl 136 100.0 1208 9 US-09-96-740-16 Sequence 16, Appl 136 100.0 1208 13 US-10-671-242-16 Sequence 16, Appl 136 100.0 1208 13 US-10-023-529-16 Sequence 16, Appl 136 100.0 1208 13 US-10-023-529-16 Sequence 16, Appl 136 100.0 1245 13 US-10-023-529-16 Sequence 16, Appl 136 100.0 16.44 13 US-10-102-806-247 Sequence 45, Appl 136 100.0 16.44 13 US-10-102-806-247 Sequence 45, Appl 136 100.0 16.44 13 US-10-023-529-45 Sequence 45, Appl 136 100.0 16.44 15 US-10-671-740-50 Sequence 45, Appl 136 100.0 16.44 15 US-10-671-740-50 Sequence 50, Appl 136 100.0 12425 13 US-10-023-529-50 Sequence 50, Appl 136 100.0 12425 13 US-10-023-529-37 Sequence 37, Appl 136 100.0 12425 13 US-10-023-529-37 Sequence 12, Appl 136 100.0 12425 13 US-10-023-529-37 Sequence 12, Appl 136 100.0 12425 13 US-10-023-529-37 Sequence 12, Appl 136 100.0 12425 13 US-10-023-529-13 Sequence 13, Appl 136 100.0 12425 13 US-10-023-529-13 Sequence 13, Appl 136 100.0 12425 13 US-10-023-529-13 Sequence 13, Appl 136 100.0 12425 13
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## ALIGNMENTS

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Law, Simon W.
Arjona, Anibal A.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPODROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
```

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APPLICATION: APPLICATION APPLICATION NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: MOVEL LOW DENSITY USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
DB:
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US-09-976-740-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
APPLICANT: Lees, Romon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 66/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION UNMBER: 15,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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No.:
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SEQUENCE DESCRIPTION: SEQ ID NO
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APPLICATION NUMBER: US/09/962,055
EILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
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CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/99/616,289
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 1200-07-07
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, App
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
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                                                                                  1 GluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
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 GAAGTGCCCGAGAGTGAC 78
                                                             GAAGTGCCCGAGAGTGAC 78
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Law, Simon W.
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Matches:
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Mismatches:
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Matches:
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: Azjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION UNMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/9/616,289
PRIOR APPLICATION NUMBER: US/9/616,289
PRIOR APPLICATION NUMBER: US/9/517,849
PRIOR APPLICATION NUMBER: US/9/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/979,608
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CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 1900-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR PRIOR PRICING DATE: 1996-11-27

PRIOR PRICING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03
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Best Local Similarity:
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; ORGANISM: Homo sapiens
US-10-023-529-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/10023523 Publication No. US20020152485A1 GENERAL INFORMATION:
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LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIA
TITLE OF INVENTION: ATHEROSCLEROSIS
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Law, Simon W.
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Matches:
Conservative:
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                                                       US-09-976-740-20 (1-26) x US-10-616-187-31 (1-78)
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                         Pred. No.:
                                                                                                        Alignment Scores:
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US-10-616-187-31
                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR PPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
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US-10-616-187-31
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DB:
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Best Local Similarity:
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US-10-023-523-31
                                                                                                                                                                                         SOFTWARE: Fas
SOFTWARE: Fas
; SEQ ID NO 31
FUNCTH: 78
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LENGTH: 78
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW BENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version
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to. US20040013668A1
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Conservative:
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Indels:
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Gaps:
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Matches:
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1 GluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,055

FILING DATE: 24-5ep-2001

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: 08/979,608

FILING DATE: 27-NOV-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: MYSSES, LOUIS

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECHMUNICATION INFORMATION:

TELEPACK: 617/542-8906

INFORMATION FOR SEQ ID NO: 16:

INFORMATION FOR SEQ ID NO: 16:
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US-09-962-055-16
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                                                              US-09-976-740-20 (1-26) x US-09-962-055-16 (1-1208)
                                                                                                  Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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Patent No. US200200520
GENERAL INFORMATION:
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COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDLING PROTEINS AND THEIR USES
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                   LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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320020052033A1
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Indels:
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING ANI TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION UMBER: US/10/671,242

CURRENT APPLICATION UMBER: US/99/616,289

PRIOR APPLICATION UMBER: US/99/616,289

PRIOR FILING DATE: 2000-07-14
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-976-740-16
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US-09-976-740-16
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CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                              Sequence 16, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 16
LENGTH: 1208
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING.
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober
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Matches:
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-529-16
                                                                                                                                                                                          APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Manibal A.

ITITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEO ID NOS: 53

NUMBER OF SEO ID NOS: 53
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PRIOR FILING DATE: 2000-03-02
PRIOR PPLICATION NUMBER: US 08/979,608
PRIOR PLING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
PRIOR I 1208
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US-10-023-529-16
VS-10-023-529-16, Application US/10023529
Requence 16, Application US/20020129388A1
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Pred. No.:
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; LOCATION: (1)...(651)
US-10-671-242-16
                                                                                                                              SOFTWARE: Fast
SEQ ID NO 16
LENGTH: 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober APPLICANT: Law, Simon | APPLICANT: Arjona, Anil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert S.
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APPLICANT: Lees, KODERL S.

APPLICANT: LAW, Simon W.

APPLICANT: LAY, Simon W.

APPLICANT: ATJONA, ANIDAI A.

FITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

FRIOR APPLICATION NUMBER: US/09/616,289

FRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1996-11-27

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 1208

TYPE: DNA
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                ; CRGANISM: Homo sapiens FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)...(651) US-10-023-523-16
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                               21 GluValProGluSerAsp 26
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No. US20020152485A1
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Conservative:
Mismatches:
Indels:
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RESULT 12

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/99,608
PRIOR APPLICATION NUMBER: US 08/99,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SECTION 61 WATER OF WEIGH A 0
                                                                 APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
FRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NOS: 846
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Best Local Similarity:
Query Match:
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US-10-102-806-247
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-616-187-16
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                                                                                                                                                                                                                                                                                                                                                          Sequence 247, Application US/10102806 
Publication No. US20030054421A1 
GENERAL INFORMATION:
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 247
LENGTH: 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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; Sequence 45, Application US/09976740
; Publication No. US20070194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
                                                                                                       RESULT 15
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Best Local Similarity:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/945,527
CURRENT FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (26)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc feature
LOCATION: (1336)
OTHER INFORMATION: n equals a,t,g, o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20030055588Alel Nucleic Acid Molecules Encoding
TITLE OF INVENTION: Nucleic Acid and Protein Homologs
FILE REFERENCE: 35800/237985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1445
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                              154 GAAGTGCCCGAGAGTGAC 171
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APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROCESING AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROCESING AND TREATING
TITLE OF INVENTION: APPLICATION FOR THEIR USE IN DIAGNOSING AND TREATING
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-10-26
PRIOR PILING DATE: 1997-10-26
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
PRATURE: CDS
LOCATION: (1)...(1614)
                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: March 13, 2004, 04:26:14
Job time : 38.6157 secs
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-Q-fggn2_1/USPTO_Spool_p_/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -QFWT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS-bits -START=1 -END=-1 -NATRIX-blosun62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09976740 @CGN 1 1 10232 @runat 10032004 094548 19551 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG-SCORE50 - WAIT -DSPBLÖCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Maximum DB
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Ygapop 10.0 , x
Fgapop 6.0 , F
Delop 6.0 , E
     27513289 seqs, 14931090276 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
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#### 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AA765474 LOCUS DEFINITION

ORGANISM

a03d01.sl NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1303873 3' similar to contains Alu repetitive element;contains element MER22 repetitive element; mRNA sequence.

A2765474 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AA765474.1 GI:2816712

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REFERENCE
AUTHORS
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 269.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                      Homo sapiens (human)
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1136 Std Error: 0.00
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 274)
                                                                                                                                                                                                                                                                                                                                    BI004562
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//clone lib="NCI CGAP GCBC CCAP GCBAP GCBAP
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/mol type="mRNA"
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/lab_host="DH10B"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=WR4&t2=NR4-HN0054-070301-002-g04&t3=2001-03-07&t4=1)
Seq.primer: puc 18 forward
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similar to
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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High quality sequence stop: 274.
Location/Qualifiers
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Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    AA806888
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                                                                sapiens (human)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Torgan: head_normal; Vector: Patent application
/note="Torgan: head_normal; Vector: Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                        275 bp. mRNA linear EST 07-APR-1998
NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1351450 3'
contains element TAR1 repetitive element :. mRNA
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                                                                                                                              RESULT 4
AA810871
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DB:
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Best Local Similarity:
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cDNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1112

Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 229.

Location/Qualifiers
             Homo sapiens (human)
                                                                     AA810871
                                                                                                  AA810871 278 bp mRNA linear EST 19-EB-1998 ob64905.sl NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1336184 3' similar to contains element PTR7 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                         AA810871.1
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                                                                                                                                                                                                                                                                GluGluGluGluAspAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
                                                                                                                                                                                       GAAGTGCCCGAGAGTGAC 162
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/clone="IMAGE:1351450"
/tissue_type="germinal_center_B_cell"
/lab_host="DH10B"
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/mol_type="mRNA"
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AA766034
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Best Local Similarity:
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Homo sapiens
Homo sapiens
                                        sequence.
AA766034
AA766034.1 GI:2817272
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AA766034 284 bp mRNA linear EST 08-FEB-1998 ca15b09.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1305017 3' similar to contains element MER22 repetitive element;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1143 Std Error: 0.00 Seq primer: -40ml3 fwd. BT from Amersham High quality sequence stop: 269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B"
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|mol_type="mRNA"
|db_xref="taxon:9606"
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REFERENCE
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DEFINITION
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BF194967
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DB:
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                                                                    BF194967 302 bp mRNA linear EST 03-NOV-2000 7091b05.xl NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643712 3' similar to contains element TAR1 TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-Yemail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 283.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1100 Std Error: 0.00
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CDNA Library Preparation: M. Bento Soares, Ph.D.,
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Unpublished (1997
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1 (bases 1 to 284)
                             BF194967.1 GI:11081346
                                           sequence.
BF194967
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                              GAAGTGCCCGAGAGTGAC 158
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 sapiens (human)
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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US-09-976-740-20 (1-26) x BF194967 (1-302)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GluValProGluSerAsp
                                                                                                                                                                                                                                                       A1470106 322 bp mRNA linear EST 14-APR-1999 tj90g09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148832_3' similar to contains TAR1.b2 PTR5 repetitive
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 322)
1 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-romail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement. Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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Unpublished (1997)
                                                                                                                     Homo sapiens
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 324)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
Proc. Natl.
20202663
                                                   Simpson, A\cdot J\cdot Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                         QV4-CI0151-091100-522-a05
BF806978
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This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 387 Std Error: 0.00
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Contact: Robert Strausberg,
                                        sequence tags
                                                                                                  O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                        Homo sapiens
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/clone lib="Soares NSF F8 9W OT PA PS1"
/note="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with
a modified polylinker; Site=1: Not I; Site=2: Ecc RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NDHSF pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares ND2H8-9W pool 1:
758280-760583, 772104-774407 Soares NDHPA pool 1:
768280-306311, 320136-32823, 336280-32663 Soares NDHPA
Soares and M. Fatima Bonaldo."
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/mol_type="mRNA"
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lone="IMAGE:2148832"
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CI0151 Homo
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BF941758
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This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-CI0151-09100-522-a05&t3=2000-11-09&t4=1)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Micha
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 345)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                         Tumor Gene Index Unpublished (1997)
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High quality sequence stop: 324.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGTGCCCGAGAGTGAC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: colon ins; Vector: puc18; Site 1: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
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similar to contains element MER22
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1 (bases 1 to 367)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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High quality sequence stop: 325.
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Clone distribution; NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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Location/Qualifiers
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sapiens cDNA clone IMAGE:1289737 3'
ER22 repetitive element ;, mRNA
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               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 383)

1 (bases 1 to 383)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, F.F., Bagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Seq primer: -40m13 fwd. ET from A
High quality sequence stop: 366.
Location/Qualifiers
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Rua Prof.
                                                               10737800
                                                                                                           sequence tags
                                                                                                                                           Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1289737"
/tissue_type="germinal center B cell"
/lab_host="UH10B"
 Antonio Prudente 109, 4 andar, 01509-010, Sao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens'
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                                                                                                                                                                                                                                                                     Metazoa;
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                                                                                             Acad. Sci.
                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-367)
                                                                                                                                                                                                                                                                                                                                                                   383 bp mRNA linear
5 CT0045 Homo sapiens cDNA,
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Indels:
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REFERENCE
AUTHORS
TITLE
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VERSION
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AA836383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GluValProGluSerAsp
                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., Bonald, Ph.D.
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 384)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     od37b07.sl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESD/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=CM4-CT0045-180
200-512-h05kt3=2000-02-18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA836383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          AA836383.1 GI:2910702
www-bio.llnl.gov/bbrp/image/image.html
                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
Cund through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence start: 21 quality sequence stop: 312. Location/Qualifiers
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/dev_stage="Adult"
/clone_lib="CT0045"
/clone_lib="CT0045"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 bp mRNA linear EST 31-MAR NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370101 contains element PTR7 repetitive element ;, mRNA
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                         Ph.D.,
                                         Sequencing Center information can be
                                                                                                                                                                   David Allman,
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                                                                                                                             Fatima
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Query Match:
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                                                                              US-09-976-740-20 (1-26) x AA836383 (1-384)
                                                                                                                               Percent Similarity:
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136 GAAGTGCCCGAGAGTGAC 153
           21 GluValProGluSerAsp 26
                                       1 GluGluGluGluAspAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop:
                                                                                                                                                                                               constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:1370101"
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Indels:
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                                       135
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RESULT 13
AW594381
LOCUS
DEFINITION REFERENCE AUTHORS TITLE ACCESSION VERSION SOURCE KEYWORDS AW594381 397 bp mRNA linear EST 22-MAF hg68e08.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2950790 similar to contains PTR5.tl PTR5 repetitive element;, mRNA Eukaryota, Metazoa; Mammalia, Eutheria, 1 (bases 1 to 397) Homo sapiens sequence. AW594381 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy AW594381.1 Homo sapiens GI:7281639 (human) Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;

EST 22-MAR-2000 E:2950790 3'

JOURNAL COMMENT

Tumor Gene Index Unpublished (1997)

Project (CGAP),

Euteleostomi;

Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk,
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, I

Ph.D., ĭ.∪.,

3 Ph.

.D., Michael

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
Cound through the I.M.A.G.E. Consortium/LLNL at:

Sequencing Center information can be

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REFERENCE
AUTHORS
TITLE
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AW134620
LOCUS
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DB:
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 82-33,

>GC_rich#Low_complexity 143-219, >(GAA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20
                                             Seq prime POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW134620
412 bp mRNA linear EST 28-OCT-
UI-H-BI1-abo-f-08-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2712710 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 397.
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                                                                                                                                                                                                                                                                                                          Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 412)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1257096-1258631, 1469664-1470983, and 1475592-1476743). Subtraction by Bento Scares and M. Fatima Bonaldo. "
Location/Qualifiers
1. .412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2950790"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                              21 GluValProGluSerAsp 26
                                                                                                                                                  AI097526 429 bp mRNA linear EST 26-OCT-1998 qb87g10.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone gb87g10.x1 samilar to contains TAR1.b2 PTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GluGluGluAspAspAspGluAspGluAspGluAspAspValSerGluGlySer 20
                                                                                          element ;, mRNA sequence.
Homo sapiens (human)
                                                                  AI097526.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2/12/10"
/clone lib="NCI GGAP Sub3"
/clone library derived from library which is a subtracted library derived from library derived from library which is a subtracted library derived from library derived from library which is a subtracted library derived from library libraries was used as a cracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI CGAP Kid3, NCI CGAP GG4, NCI CGAP Exid5, NCI CGAP Kid5, NCI CGAP Shr33, 3021 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1323912-1328831, 1471368-1472903, 1492104-1493255); NCI CGAP Kid5 pool 1 LLAM 338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1328831, 1471368-1472903, 1492104-1493255); NCI CGAP Lub pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1323912-1328831, NCI CGAP Pr22 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 986795, 1101122-1101959, 1217928-1222615); NCI CGAP 986795, 1101122-1101959, 1217928-1222615); NCI CGAP 986795, 1101123-1101959, 1217928-1222615); NCI CGAP 986795, 1101123-1101959, 1217928-1220615); NCI CGAP 986796.

TAG TIRSUTE LEAM 370-28670 (10 MAGE CloneIDs 10 MAGE CloneIDs 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_TISSUE=brain
TAG_LIB=NCI_CGAP_L
TAG_SEQ=ATAGG"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2712710"
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Matches:
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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

RESULT 15 AI097526 LOCUS

DEFINITION

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Score: Pred. No.: ORIGIN

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity:
Query Match:
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Search completed: March 13, 2004, 04:01:36 Job time: 393.119 secs
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                       GAAGTGCCCGAGAGTGAC 236
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//lab host="DH10B (ampicillin resistant)"
//clone_lib="Soares_fetal_heart_NbHH19W"
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:1707138"
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-Q=/Ggn2_1/USPTO_Spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmb1 -QFMT-fastap -SUFFIX=rge -MINTATCH=0.1 -LOOPCE=0 -LOOPEXT=0
-UNITS-blits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXI=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEPLOTX=7
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Ygapop 10.0 , Ygapext
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29: em_vi:*
30: em_htg_hum:*
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36: em_htg_mam:*
37: em_htg_mam:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# | Result | Match tempth DB | ID | Description | Descriptio

RESULT 1

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RESULT 3
AR409327
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AR374692
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6605588-A 32 12-AUG-2003;
Location/Qualifiers
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Lees,A.M., Lees,R.S., Law,S.W. and Arjor
Low density lipoprotein binding proteins
diagnosing and treating atherosclerosis
Patent: US 6359451-A 32 12-MAR-2002;
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                                                                                                                                                                                                                       /mol_type="genomic DNA"
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RESULT 5
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Location/Qualifiers
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6632923-A 32 14-OCT-2003;
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Low density liprotein binding proteins and their use in diagnosing
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33 bp DNP density lipoprotein binding
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/mol_type="unassigned DN
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PAT 18-DEC-2003

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1 (bases 1 to 3)

2 Lees,A.M.; Lees,R.S., Law,S.W. and Arjona,A.A.

Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

AL Patent: JP 2001506983-A 12 29-MAY-2001;

BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/12

PN JP 2001506983-A/12

PP 26-MOY-1997 JP 1998524870

PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC C07K21/00, C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC Topology: Linear; CC Topology: C
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Lees, A.M., Lees, R.S.,
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AR199546
AR199546.1 GI:20249620
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Aequorea victoria
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BD056454
BD056454.1 GI:22602060
JP 2001506983-A/12.
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1 (bases 1 to 36)

Low density lipoprotein binding proteins and the diagnosing and treating atherosoclerosis

Low density 13 6605588-A 38 12-AUG-2003;

Location/Qualifiers
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AR409333
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6632923-A 38 14-OCT-2003;
Location/Qualifiers
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         RS Lees, M., Lees, R.S., Law, S.W. and Arjona, A.A.

Novel low density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis
aL Patent: JP 2001506983-A 18 29-MAY-2001;
BOSTCON HEART FOUNDATION INC
PN JP 2001506983-A/18
PD 29-MAY-2001
PF 26-NOV-1997 US 60/031930, 03-UUN-1997 US 60/048547 PI
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC
A61X38/04, A61X38/17, A61X39/00, A61X48/00, A61X49/00, A61X49/00, A61X51/08, PC
C07H21/00,
C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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AX239595
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Patent: WO 0164874-A 38 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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1 (bases 1 to 36)
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JP 2001506983-A/18.
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Low density liprotein binding proteins and their use in diagnosing
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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RESULT 11
AR199539
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                             Le (bases 1 to 78)
Lew S.A.M., Lees, R.S., Law, S.W. and Arjona, A./
Low density lipoprotein binding proteins and
diagnosing and treating atherosclerosis
Patent: US 6605588-A 31 12-AUG-2003;
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Sequence 31 from patent US
AR374691
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their
diagnosing and treating atherosclerosis
Patent: US 6355451-A 31 12-MAR-2002;
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RESULT 13
AR409326
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AR409326

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US-09-976-740-21 (1-11) x AR374691

(1-78)

Percent Similarity:
Best Local Similarity:
Query Match:

0.00694 54.00 100.00% 100.00% 100.00%

Alignment Scores:

. No.:

ORIGIN

mol\_type="genomic

B

46

REFERENCE AUTHORS TITLE

1 (bases 1 to 78) Lees, A.M., Lees, R.S.,

FEATURES

source

/organism="unknown" /mol\_type="genomic | Location/Qualifiers

JOURNAL

KEYWORDS SOURCE ORGANISM

Unknown

Unclassified.

VERSION

Sequence 31 AR409326 AR409326.1

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1 ValSerGluGlySerGluValProGluSerAsp
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                                           Patent: WO 0164874-A 31 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
                                                                                           Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.

Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      AX239588 78 bp Sequence 31 from Patent WO0164874. AX239588
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Low density. Lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 6632923-A 31 14-OCT-2003;
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from patent US 6632923.
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BD056453
LOCUS
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Best Local Similarity:
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CE 1 (bases 1 to 78)

Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

RS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

ROVel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

Patent: JP 2001506983-A 11 29-WAY-2001;

BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/11

PD 29-MAY-2001

PF 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI 29-MAY-2099 JP 1998524870

PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC AGIX38/04, AGIX38/17, AGIX39/00, AGIX48/00, AGIX49/00, AGIX51/08, PC C07H21/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC Strandedness: Single; CC Topology: Linear; Location/Qualifiers.
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Novel low density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis,.
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Aequorea victoria
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BD056453.1 GI:22602059
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REFERENCE AUTHORS TITLE

FEATURES

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KEYWORDS SOURCE ORGANISM

Homo sapiens (human)

DEFINITION ACCESSION RESULT 14 AX239588 LOCUS

VERSION

AX239588.1 GI:15797264

뭉 8 Percent Similarity:
Best Local Similarity:
Query Match:
DB:

0.00694 54.00 100.00% 100.00% 100.00%

Alignment Scores:

US-09-976-740-21 (1-11) x AR409326 (1-78)

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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1: geneseqn1980s:*
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Fgapop 6.0 , Fgapext
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                                                             (BOST-) BOSTON HEART FOUND INC
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                                                  Sequence 78
                                                                                                                                                                                                                                 Disclosure; Page 9; 143pp; English.
                                                                                                                                                                                                                                                          diagnosing and/or
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                    ValSerGluGlySerGluValProGluSerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lees RS,
                                                                                                                                                                                                                                                                                                                                                                    Page 10; 143pp; English.
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2000US-00616289.
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                                                                                                                                                                                 22 A; 16 C;
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Conservative:
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RESULT 5
AAV32838
AID VARA93
AX AAV3
AX AAV3
AX AAV3
AX Low
KW Low
KW Low
KW Low
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KW Meey
FH CDS
FH Misc

                                                                            This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-2 (see AAW49041). It was isolated by screening human liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA clones (see AAW2934-9) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerotic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subjects at risk.
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03-JUN-1997;
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                                                         and host cells used to produce recombinant
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DB; AAW49041.
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67. .99
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97US-0048547P.
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Alignment Scores: Pred. No.:

0.463

Length

1208

Sequence 1208 BP; 252 A; 368 C; 321 G; 266

T; 0 U; 1 Other;

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RESULT 6
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14-JUL-2000; 2000US-00616289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
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The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were isolated from human foetal brain, liver and aorta cDNA libraries using rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in AAH26499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods are thereselerosis, methods for treating an agent for use in treating atherosclerosis, methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LB are also claimed LBP polypeptide or nucleic acid, and vaccine

Example

Fig 16; 143pp;

English.

BP; 252 Þ 368 Ç 321 <u>و</u> 266 T; 0 U; 1 Other,

Alignment Scores:

Query Match: DB: Ś Percent Similarity: Best Local Similarity: US-09-976-740-21 Pred. No.: (1-11)100.00% 100.00% 100.00% x AAH26494 0.463 (1-1208)Mismatches: Indels: Gaps: Length: Matches: Conservative: 11 1208 11

맑 67 ب GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC ValSerGluGlySerGluValProGluSerAsp 99

RESULT AAF21860

AAF21860 standard; DNA; 1336 ВP

AAF21860;

27-MAR-2001 (first

Human breast and ovarian cancer associated antigen gene SEQ ID 247.

Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.

WO200055173-A1

21-SEP-2000

08-MAR-2000; 2000WO-US005881

12-MAR-1999; 99US-0124270P

(HUMA-) HUMAN GENOME SCI INC

Rosen CA,

WPI; 2000-611515/58. P-PSDB; AAB58957.

New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatme and diagnosis of cancer, immune disorders, cardiovascular disorders as neurological diseases disorders and

Claim 1; Page 670-671; 1299pp; English

Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB58711 - AAB59128. The DNA and protein sequences are CC associated with breast and ovarian cancer. Included in the invention are Sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist cor antagonist sequences exhibit cytostatic; immunosuppressive; noctropic; cc neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; cantifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly corporate and ovarian cancer. The nucleic acid sequences, proteins, agonists and ovarian cancer. The nucleic acid sequences, proteins, agonists cof immune disorders e.g. Addison's disease, altroimmune condities, rheumatoid arthritis and ulcerative colitis; cc cardiovascular disorders such as myocardial ischaemias; wound healing;

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RESULT 8
AAH26489
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Best Local Similarity:
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The present sequence is that of cDNA encoding a portion (see AAB82799) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an
                                                                                                                                                                                                                                                                                                                                               02-MAR-2000;
14-JUL-2000;
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                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA
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DB; AAB82799.
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                                                                                                                                                                                                                                                                                           Lees RS,
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                                                                                                                                                                                                                                                                                            Arjona AA
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Gaps:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1362 BP; 259 A; 421 C; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, a compositions, are also claimed
                                                                                                                                   New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                           WPI; 2001-565505/63.
                                                                                                                                                                                                                                  02-MAR-2000; 2000US-00517849: 14-JUL-2000; 2000US-00616289:
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                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                              Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
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The present sequence is that of cDNA encoding a portion (see AAB82800) of novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in AAH26491. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well ass expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent

Example 2; Fig 13; 143pp; English.

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The present sequence is that of the coding region of the human gene (see also AAH26494) encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB2806). The gene was isolated from a genomic DNA library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the present sequence differs from that predicted from a cDNA clone (see AAB2803) in that it contains an additional 321 amino acids at its N-terminus (the cDNA is a 5' truncation). LBP-2 mucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are capable of binding to native and methylated LDL. Also claimed are consisted LBP polypeptides, and biologically active fragments and capacities of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for revaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine
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14-JUL-2000; 2000US-00616289.
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DB; AAB82806.
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py; diagnosis;
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WPI; 1998-322455/28
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                                                                                                                                                                                                                                                                                                                                          Rabbit low density lipoprotein binding protein LBP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
                Lees AM,
                                             27-NOV-1996;
03-JUN-1997;
                                                                    26-NOV-1997;
                                                                                  04-JUN-1998.
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                               HEART FOUND INC
                                             96US-0031930P.
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                   02-MAR-2000; 2000US-00517849
14-JUL-2000; 2000US-00616289
                                                                          28-FEB-2001; 2001WO-US006356
                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                       Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA
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                                                                                                                                                WO200164874-A2
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The present sequence is that of cDNA encoding a portion (see AAB82798) of convel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA convel rabbit low density lipoprotein 2 (LBP-2). The cDNA converse are converted following screening arabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions compositions and LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
    Sequence 1617 BP; 289 A; 513 C; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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Query Match: DB: US-09-976-740-21 (1-11) x AAH26488 (1-1617) Best Local Percent Similarity: No. . Similarity: 0.645 54.00 100.00% 100.00% Matches: Conservative: Mismatches: Indels: Length 11 1617 11 0 0

364 1 ValSerGluGlySerGluValProGluSerAsp GTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGAT 396

RESULT 13 AAH26500 AAH26500 standard; cDNA; 2561 ВP

Rabbit low density lipoprotein binding protein 2 (LBP-2) CDNA

12-NOV-2001

(first entry)

AAH26500;

Oryctolagus Low density lipoprotein binding protein atherosclerosis; antiarteriosclerotic; g cuniculus gene 2; LBP-2; LDL; rabbit; gene therapy; diagnosis; vaccine;

/\*tag= Location/Qualifiers ρι

WO200164874-A2

28-FEB-2001; 2001WO-US006356

02-MAR-2000; 14-JUL-2000; 2000US-00517849 2000US-00616289

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 1 (LBP-2, see ALBR3807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 2A; 143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH82494). The open reading frame spans 5 sxons. Human LBP-2 cDNA (see acids are among claimed polymucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for evaluating an acell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
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                                       Novel human polynucleotide, SEQ ID NO: 603
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14-JUL-2000; 2000US-00616289.
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Human, cytostatic; gene therapy; colon cancer; prostate cancer; breast cancer; lung cancer; cancer detection; ss.
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12425 BP; 2563 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of genomic DNA encoding novel human
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                                                                                                                              standard; cDNA; 378 BP
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                                                                                                                                                                                                                                                                                  CC The present sequence is one of 3351 sequences in a library of human CC polynucleotides. The library is used to detect differentially expressed CC genes correlated with a cancerous state of a mammalian cell and can CC detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies CC of the polynucleotides. The probes can be used for chromosome mapping of CC or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in CC their gene products are used as genetic or biochemical markers (e.g. in CC carcinogenesis pathway and/or monitor the earliest changes along the CC carcinogenesis pathway and/or monitor the efficacy of therapies and CC preventive interventions. The polynucleotides, polypeptides and CC preventive interventions. The polynucleotides, polypeptides and CC treat the cancers and proliferative disorders such as neoplasia, CC dysplasia and hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamso:
Drmanac R, Crkenjakov R, Drmanac S, Dickson M, Labat I;
Leshkowitiz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
                                                                                                                                                                                                                                                     Sequence 378 BP; 95 A; 95 C; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences.
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN 1 1 235 @runat 10032004 094549 19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGE_SCORESO -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOD=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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-MODEL=frame+_p2n.model -DEV=xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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100.0
100.0
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  March 12, 2004, 20:05:17; Search time 3.7295 Seconds (without alignments) 1636.805 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                  Length
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US-08-979-608A-32

US-09-517-849-32

US-09-616-289-32

US-08-979-608A-38

US-09-517-849-38

US-09-616-289-38

US-08-979-608A-31

US-09-517-849-31

US-09-616-289-31

US-09-517-849-37

US-09-517-849-37

US-09-516-289-37
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                                 Sequence 32,
Sequence 32,
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Sequence 38,
Sequence 31,
Sequence 31,
Sequence 31,
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US-08-979-608A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees.
                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lees,
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## ALIGNMENTS

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Sequence 32, Application US/08979608A
Patent No. 635451

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Lees, Ann M.
FITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILLING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
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NAME/KEY: Coding Sequence
LOCATION: 1...33
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-979-608A-32
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-517-849-32
Sequence 32, Application US/09517849
Patent No. 660588
GENERAL INFORMATION:
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TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                     NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
No.:
                                                                                                                                                                                              APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: RESUSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                 ENGTH: 33 base pairs
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Law, Simon W
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Lees, Robert S.
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL NOW DENSITY DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION: NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF ESO ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 33
TYPE: DNA
ORGANISM: Homo sapiens
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                                US-08-979-608A-38; Sequence 38, Application; Patent No. 6355451; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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                                                                                                        RESULT 4
                                                                                                                                                                                                               US-09-976-740-21 (1-11) x US-09-616-289-32 (1-33)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear FEATURE:
APPLICANT: Lees,
Lees,
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5. 6632923
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                                                                        US/08979608A
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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Robert S

ADDRESSEE: Fish & Richardson P.C.

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COMPUTER: IBM CONDITION
COMPUTER: IBM CONDITION
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/79,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/ACENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 10597-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMA
                                                                                                                                                                                                                                                                                 RESULT 5
US-09-517-849-38
; Sequence 38, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
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Best Local Similarity:
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MEDIUM TYPE: Diskette
                                                         Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 38:
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CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  APPLICANT: Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C.
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Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                  Law, Simon W.
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Gaps:
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Matches:
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN AND
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN DIAGNOSING AND
TITLE OF INVENTION: ATTHENSECLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1907-01-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-616-289-38
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION NUMBER: 08/979,608
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY,AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE,DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 66329
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 38:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTGTCCGAGGGCTCGGAGGGTGCCCGAGAGCGAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValSerGluGlySerGluValProGluSerAsp 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
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Matches:
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Indels:
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US-08-979-608A-31
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Best Local Similarity:
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; ORGANISM: Homo sapiens
US-09-616-289-38
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SOFTWARE: FASI
SEQ ID NO 38
FENGTH: 36
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APPLICANT: Lees,
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                          NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/048,547 FILING DATE: 03-UN-1997 APPLICATION NUMBER: US 60/031,930 FILING DATE: 27-NOV-1996 ATTONNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                 NAME/KEY: Coding Sequence LOCATION: 1...78
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT
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CORRESPONDENCE ADDRESS:
ADDRESSEE Fish & Richardson P.C.
STREET: 225 Franklin Street
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDLING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                           FEATURE:
                                                                                                                                      LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
ENT APPLICATION DATA:
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STATE: MA
                                                                                                                 TOPOLOGY: linear
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                      SEQ ID NO: 31:
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Matches:
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Query Match:
DB:
                            Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
                                                             Score:
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Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, I
                                                                                                                                                                                                      TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRAINEDDIESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REPERENCE/DOCKST NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Law, Simon W.
Arijona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                           SEQUENCE DESCRIPTION:
                                                                                                                                                                                            FEATURE:
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/979,608 FILING DATE: 26-NOV-1997
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
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               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-976-740-21 (1-11) x US-09-517-849-31 (1-78)

COMPUTER: IBM Compatible

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DB:
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Best Local Similarity:
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US-08-979-608A-37
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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR PPLICATION NUMBER: US 60/031,930
PRIOR PPLICATION NUMBER: US 60/031,930
PRIOR PPLICATION NUMBER: US 60/031,930
PRIOR PPLICATION NUMBER: US 60/048,547
PRIOR PRICING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08979608A Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober
                                                                                                                                                                                             Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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6632.
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
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                                                                          CITY: Boston
STATE: MA
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Law, Simon W.
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54.00
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Matches:
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Indels:
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RESULT 11
US-09-517-849-37
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIDM TYPE: Diskette
MEDIDM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U8/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1...84
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 GIGICCGAGGGCTCGGAGGTGCCCGAGAGCGAT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09517849
                                                                                                                                                                                                                                                                                                                                                                                                                               Lees, Robert
Law, Simon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.00377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert S.
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Matches:
Conservative:
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Indels:
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APPLICANT: ALTONA, ANIDAI A.

APPLICANT: ALTONA, ANIDAI A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SECTIONARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-37
Query Match:
DB:
                                        Percent Similarity:
Best Local Similarity:
                                                                                Score:
                                                                                                   Pred. No.:
                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                        SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, App. Patent No. 66329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Aniba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REBERBUG/DOKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       ENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Coding Sequence LOCATION: 1...84
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/979,608 FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09616289
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                   0.00377
54.00
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                                                         Length:
Matches:
Conservative:
                   Mismatches:
Indels:
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Indels:
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RESULT 13
US-08-979-608A-16
; Sequence 16, Application
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, A
                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence;
; LOCATION: 1...651
; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-979-608A-16
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                                                                          US-09-976-740-21 (1-11) x US-08-979-608A-16 (1-1208)
                                                                                                                                   Query Match:
                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 42
67 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GTGTCCGAGGCTCGGAGGTGCCCGAGAGCGAT 84
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                      ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1208 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application
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Law, Simon W.
Arjona, Anibal A.
                                                                                                                                 100.00%
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54.00
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                                                                                                                                                                                                                                                                                            SEQ ID NO: 16:
                                                                                                                                 Conservative: Mismatches: Indels:
                                                                                                                 Gaps:
                                                                                                                                                                                           Length:
Matches:
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                                                                                                                 1208
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RESULT 14
US-09-517-849-16
; Sequence 16, Application US/09517849
; Patent No. 6605588
; Patent NO. BOOKMATION:
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US-09-616-289-16
; Sequence 16, Application US/09616289
; Patent No. 6632923
                                                                                                                                                                                                     Ś
                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                         US-09-976-740-21 (1-11) x US-09-517-849-16 (1-1208)
                                                                                                                                                                                                                                                                                                                                                             Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-517-849-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/979,608
FILLING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                    GENERAL INFORMATION:
                  APPLICANT:
                                                  APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARRE: FRAETSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 1...651 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 42
                                                                                                                                                                        67
                                                                                                                                                                                            1 ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
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Law, Simon W.
                                                                                                                                                                                                                                                                                          100.00%
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Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                            Conservative:
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                                                                                                                                                                                                                                                                          1208
11
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PRIOR PILICATION NUMBER: US 09/517,849
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
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                                   Ş
                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-616-289-16
                                                                      US-09-976-740-21 (1-11) x US-09-616-289-16 (1-1208)
                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/616,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS FILE REFERENCE: 10797-004001
67 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 99
                   1 ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                100.00%
                                                                                                                                                                                     0.0775
54.00
                                                                                                                                Conservative: Mismatches: Indels:
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Matches:
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Search completed: March 13, 2004, 04:06:26 Job time : 5.7295 secs

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Result
No.
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-MODEL=frame+ p2n.model -pUS09976740/runat 10032004 094549 19588/app query.fasta_1.1898
-Q=/cgn2 1/USPTO_spool_p/US09976740/runat 10032004 094549 19588/app query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX-100
-THR MIN=0 -ALICM=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-THR MIN=0 -ALICM=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09976740 @CGN 1 1 712 @runat 10032004 094549 19588
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEGUT=120 -WARN TIMEGUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic search, using frame_plus_p2n model
Query
Match Length DB
                                                                                                            US-09-976-740-21
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 12, 2004, 20:46:42; Search time 15.9143 Seconds (without alignments) 2544.725 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2432557 seqs, 1840798884 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VSEGSEVPESD 11
                                                                                                       1: /cgn2=6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2=6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2=6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2=6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2=6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2=6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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10: /cgn2=6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2=6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2=6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2=6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2=6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2=6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
12: /cgn2=6/ptodata/1/pubpna/US10E_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
 H
                                    SUMMARIES
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 Description
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US-09-962-055-32

US-10-976-740-32

US-10-023-523-32

US-10-023-523-32

US-10-023-523-32

US-10-023-523-32

US-10-023-523-38

US-10-023-523-38

US-10-023-523-38

US-10-023-523-38

US-10-023-523-38

US-10-023-523-38

US-10-023-523-31

US-10-023-523-31

US-10-023-523-31

US-10-023-523-31

US-10-023-523-31

US-10-023-523-37

US-10-023-523-12

US-10-023-523-13

Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 31, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl

US-09-962-055-32	
Patent No. US20020052033A1	
GENERAL INFORMATION:	
; APPLICANT: Lees, Ann M.	
Lees, Robert S.	
Law, Simon W.	
; Arjona, Anibal A.	
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN	ROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND	EIR USES IN DIAGNOSING AND
; TREATING ATHEROSCLEROSIS	33
; NUMBER OF SEQUENCES: 42	
; CORRESPONDENCE ADDRESS:	
; ADDRESSEE: Fish & Richardson P.C.	
; STREET: 225 Franklin Street	
; CITY: Boston	
; STATE: MA	
; COUNTRY: USA	
; ZIP: 02110-2804	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Diskette	
; COMPUTER: IBM Compatible	
; OPERATING SYSTEM: DOS	

ALIGNMENTS

```
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: ALTONA, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 1000-07-14
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 66/979,608
PRIOR APPLICATION NUMBER: US 66/979,608
PRIOR APPLICATION NUMBER: US 60/91,930
PRIOR FILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOSE: 53
SOFTWARE: FastSEQ for Windows Version 4.0
; ORGANISM: Homo sapiens
US-09-976-740-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
                                                                      SEQ ID NO 32
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 26-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence LOCATION: 1...33
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ValSerGluGlySerGluValProGluSerAsp 11
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100.00%
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APPLICANT: AZJONA, ANIBAL A.

APPLICANT: AZJONA, ANIBAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/671,242

CURRENT ELLING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR FILLING DATE: 2000-07-14

PRIOR FILLING DATE: 2000-07-14

PRIOR FILLING DATE: 2000-03-02

PRIOR FILLING DATE: 1907-11-26

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILLING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                   US-10-023-529-32
; Sequence 32, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                               RESULT 4
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-10-671-242-32
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                               APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal i
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober APPLICANT: Law, Simon APPLICANT: Arjona, Ani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                   1 ValSerGluGlySerGluValProGluSerAsp 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTGTCAGAGGCTCTGAAGTGCCCGAGAGTGAC 33
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Law, Simon W.
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Matches:
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Mismatches:
Indels:
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Matches:
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WESULT 5
US-10-023-32
Sequence 32, Application US/10023523
Publication No. US20020152485A1
GENERAL IMFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Low DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 1900-03-02
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-01-26
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-01-26
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-01-26
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-01-26
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR FILING DATE: 1997-01-00-01-12-17
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,849
PRIOR APPLICATION NUMBER: US 00/517,84
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CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-60-03
VUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 33
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      Score:
Percent Similarity:
                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-523-32
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Best Local Similarity:
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Length:
Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-616-187-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 33
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSEE: Fish & Richardson
ADDRESSEE: 225 Franklin Street
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RESULT 7
US-09-962-055-38
/ Sequence 38, Application US/09962055
/ Patent No. US20020052033A1
/ GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Form M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-976-740-21 (1-11) x US-10-616-187-32 (1-33)
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDLING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                          1 ValSerGluGlySerGluValProGluSerAsp 11
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No. US20040013668A1
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Matches:
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P.C.

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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lew, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REPERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US (0/031,930)

PRIOR APPLICATION NUMBER: US (0/031,930)

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR PILING DATE: 1996-11-27

PRIOR FILING DATE: 1997-06-03
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Best Local Similarity:
Query Match:
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US-09-976-740-38
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Publication No. US20020194633A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION UNBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-002001 (formerly 3983/59818)
TELECHMUNICATION: TELECHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence LOCATION: 1...36 SEQUENCE DESCRIPTION: SEQ ID NO
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09976740
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Lees, NOUSE, APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ITILE OF INVENTION: NOVEL LOW DENSITY SET IN DIAGNOSING AND
ITILE OF INVENTION: ATHEROSCLEROSIS
ITILE OF INVENTION: NOWBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SED ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ I DNO 38
LENGTH: 36
                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-740-38
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Best Local Similarity:
Query Match:
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                                                                          US-09-976-740-21 (1-11) x US-10-671-242-38 (1-36)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lees, Ann M. APPLICANT: Lees, Robert S.
                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GTGTCCGAGGCTCGGAGGTGCCCGAGAGCGAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ValSerGluGlySerGluValProGluSerAsp
                        ValSerGluGlySerGluValProGluSerAsp
GTGTCCGAGGCTCGGAGGTGCCCGAGAGCGAT 36
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10. US20040040049A1
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Matches:
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Sequence 38, Application US/10023529; Publication No. US20020129388A1; GENERAL INFORMATION:

RESULT 10 US-10-023-529-38

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US-10-023-523-38

Sequence 38, Application US/10023523

Publication No. US20020152485A1

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILLE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,523

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOPTWARE: PRESEQ FOR Windows Version 4.0

SEQ ID NO 38

LENGTH: 36

TYPE: NAA
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Narjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILLE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT PAPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 36
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-38
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: APHEROSCILEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOSTWARE: FASESEQ for Windows Version 4.0
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US-10-616-187-38
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US-09-962-055-31
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                                                                      Sequence 31, Application US/09962055
Patent No. US20020052033A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 38
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 36
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                             1 ValSerGluGlySerGluValProGluSerAsp 11
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Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
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Matches:
Conservative:
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TYPE: DNA

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Alignment Scores:

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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-976-740-31
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GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS

TILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT PILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                Sequence 31, App
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
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No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION UNMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 1...78
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         4
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CITY: Boston
STATE: MA
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches:
Conservative:
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FILE OF INVENTION:
FILE REFERENCE: 10797-004001
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 10900-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-671-242-31
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LENGTH: 78
TYPE: DNA
ORGANISM: Homo sapiens
US-09-976-740-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W. A.
APPLICANT: Law, Simon W. A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
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1 ValSerGluGlySerGluValProGluSerAsp
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age

Db 46 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 78
Search completed: March 13, 2004, 04:26:14
Job time: 15.9143 secs

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Command line parameters:

-MODEL=frame+_D2n.model -DEV=xlp
-Q=/c9n2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-Q=/c9n2_1/USPTO_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DE-CTALIGN=200-THR_SCORE=pet -MATRIX=blosum62_-TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pet -THR_MAX=100 -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXIEN=2000000000
-USER=US09976740_@CGN_1_1_10232_@runat_10032004_094548_19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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54
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     27513289 seqs, 14931090276 residues
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(c) 1993 - 2004 Compugen Ltd
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### 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.

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Query Match

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AW490346 UI-M-BH AW490346 UI-M-BH I102597 EST21188 I379283 tc73b06. W016794 UI-H-BI0 AW531666 UI-R-C4 BE199810 ug7Jb07 BE199810 ug7Jb07 BE19673 qe28f06.	30441 EST227116 30446 EST227191 134620 UI-H-BII 470100 UI-M-BHI 4701363 EST199862 44363 EST19987 97526 qb87910.x 97526 qb87910.x 97526 qb87910.x	70106 tj99099. 70106 tj99099. 806978 QV4-CI0 100558 UI-R-BJ 112745 UI-R-CD 561482 UI-R-C2 11665 UI-R-C2 72508 UI-R-C3 72508 UI-R-C3 72508 UI-R-C3 72505 nad92h0 48990 UI-R-C3 114632 UI-R-C3 11516 UI-R-C3 165164 0a24a07 165164 0a24a07 165164 0a24a07 165164 0a24a07 165164 0a24a07	807020 cc30g04.s 713567 UI-R-AG1- 029068 zk09h07.s 705474 ca033d17.s 1004562 MR4-HN00 806888 cc32g06.s 810871 cb64g05.s 766034 ca15b09.s 8766034 ca15b09.s 804533 ns28c06.s

## ALIGNMENTS

ACCESSION VERSION KEYWORDS	RESULT 1 AA807020 LOCUS DEFINITION
2 2 2 2 2 2	

SOURCE ORGANISM sequence.
AA807020
AA807020.1
EST. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo Homo sapiens AAB07020 222 bp mRNA linear EST 07-APR-1998 oc30g04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1351254 3' similar to contains element MSR1 repetitive element ;, mRNA GI:2876596 (human)

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RESULT 2
AI713567
LOCUS
DEFINITION
 REFERENCE
AUTHORS
TITLE
                                                                                               SOURCE
ORGANISM
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VERSION
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                          124 GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 156
                                                                                                                                             AI713567 253 bp mRNA linear I
UI-R-AG1-aan-a-08-0-UI.sl UI-R-AG1 Rattus norvegicus
UI-R-AG1-aan-a-08-0-UI 3', mRNA sequence.
AI713567 AI713567.1 GI:5017367
               1 (bases 1 to 253)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1153 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 211.
Location/Qualifiers
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                Rattus norvegicus
                                                                                                            Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 222)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   Normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonaldo,
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/db_xref="taxon:9606"
/clone="IMAGE:1351254"
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                  Lennon, G.
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                  Soares, M.B.
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s cDNA clone
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 269)
                                                                                                                                                                                                                                                AA029068 269 bp mRNA
zk09h07.s1 Soares_pregnant_uterus_NbHPU
IMAGE:470077 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smail: bento-soares@ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
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/dev stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="PH10B (Life Technologies)"
/clone lib="U-R-AG1"
/clone lib="U-R-AG1"
/clone return for the UI-R-AG1
/polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AG1
library is a normalized library constructed from 13 dpc
rat ventricle. The tag is a string of 6 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Lennon and Soares, Genome Research 6: 791-806, 1996.
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TAG_LIB=UI-R-AG1
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/strain="Sprague-Dawley"
/db_xrefs="taxon:10116"
/clone="UI-R-AG1-aan-a-08-0-UI"
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/mol_type="mRNA"
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          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 271)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                    AA765474.1 GI:2816712
EST:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Insert Length: 1135 Std Error: 0.00
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Contact: Wilson
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                                                                                                          Homo sapiens
                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                             ValSerGluGlySerGluValProGluSerAsp
                                                                                                                                                                                                                                                                                                                                         GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC
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314 286 1810
Gene Index
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/mol type="mRNA"
/db_xref="GDB:3756079"
/db_xref="taxon:9606"
/clone="IMAGE:470077"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
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/lab_host="DH10B"
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                             Homo sapiens (human)
Homo sapiens
Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 274)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Erentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                           274 bp mRNA linear
MR4-HN0054-070301-002-g04 HN0054 Homo sapiens cDNA,
EI004562
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1136 Std Error: 0.00

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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
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Contact: Robert St
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High quality sequence ston. 250
sequence tags
                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                          BI004562.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="germinal center B cell"
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/clone="IMAGE:1303873"
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                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AA806888 275 bp mRNA linear EST 07-APR-1998 oc32g06.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351450 3' similar to contains element TAR1 repetitive element ;, mRNA
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20202663
10737800
                                               Ph.D., Gerald Martı, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                         1 (bases 1 to 275)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                           AA806888.1 GI:2876464
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                         cDNA Library Arrayed by: Greg Lennon, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 174
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                            David Allman,
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RESULT 7
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                                                                                                                                      Ph.D., Gerald matti, ..... M. Bento Soares, cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 278)
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National Cancer Institute, Cancer Genome Anat
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Sonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NCI CGAP GCB1"
//clone lib="NCI CDAP GCB1"
//clone lib="NCI CDAP GCB1"
//clone lib="NCI CDAP GCB1"
//clone lib="NCI CGAP GCB1"
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/lab_host="DH10B"
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/mol_type="mRNA"
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/clone="IMAGE:1351450"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                    Ph.D.,
                                                                                                                                                                         Ph.D.,
                                            Sequencing Center information can be
                                                                                                                                                                                                                                       David Allman,
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AA766034
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Best Local Similarity:
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Bonald. Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Ayrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html
Insert Length: 1100 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham
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                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA766034 284 bp mRNA linear EST 08-FEB-
oa15b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1305017
similar to contains element MER22 repetitive element ;, mRNA
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National Cancer Institute, Cancer Genome Anat
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AA766034
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Insert Length: 1143 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 269.
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/db_xref="taxon:9606"
/clone="IMAGE:1336184"
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|mol_type="mRNA"
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Mismatches:
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                                                                                                                                                                                                    David Allman,
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similar to
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 271.

Location/Qualifiers
                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ValSerGluGlySerGluValProGluSerAsp
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 289)
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                        Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC 158
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAGE:1305017"
/tissue_type="germinal center B
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 bp mRNA linear EST 18-FEB-1998 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184938 3' contains element MER22 repetitive element ;, mRNA
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                                                                                                                                                                       Ph.D.,
                                                                                                                                                                                                         David Allman,
                                                                                                                                                                       M. Fatima
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RESULT 10
AI137809
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALL3/BUY
UI-R-CO-hz-h-01-0-UI.$1 UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-hz-h-01-0-UI 3', mRNA sequence.
AT137800
                           TEL: 319 335 8250

Fax: 319 335 8250

Email: bento-soares@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through The following repetitive elements were found in this cDNA sequence: 93-134, >GC_rich#Low_complexity 135-216,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                University of Iowa
375 Newton Road , '
                                                                                                                                                                                                                                                                     Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 302)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
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>(GGA)n#Simple_repeat
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                            Contact: Soares, MB
                                                                                                                                                                                                                                                                                                               8889548
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1184938"
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/lab_host="DH10B"
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SOURCE KEYWORDS VERSION ACCESSION ORIGIN

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BF194967
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7091b05.x1 :
similar to
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1 (bases 1 to 302)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Proje
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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/ clone | 11b="UIR-CO"
/ clone | 11b="UIR
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="UI-R-CO-hz-h-O1-O-UI"
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 bp mRNA linear EST 03-NOV-2000 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643712 3' contains element TAR1 TAR1 repetitive element ;, mRNA
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Indels:
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          Ph.D., Micha
on: M. Bento
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JOURNAL COMMENT
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AUTHORS
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AI470106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 387 Std Error: 0.00 Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                                                                                                                                AI470106.1 GI:4332196
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 bp mRNA linear BST 14-APR-1999 tj90g09.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:2148832 3' similar to contains TAR1.b2 PTR5 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              AI470106
                                                                                                                                                                                                                                                                          Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValSerGluGlySerGluValProGluSerAsp
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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clone lib="Soares NSF F8 9W OT PA P S1"
note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.97
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                                                  lone="IMAGE:2148832"
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                                  host="DH10B"
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Conservative:
Mismatches:
Indels:
Gaps:
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US-09-976-740-21 (1-11) x A1470106
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Best Local Similarity:
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1 (bases 1 to 324)

Dias Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ы
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-CI0151-091100-522-a05&t3=2000-11-09&t4=1)
                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF806978 324 bp mRNA linear QV4-CI0151-091100-522-a05 CI0151 Homo sapiens cDNA,
                                                                                                                                                                                 Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                Brazi
                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                        +55-11-2707001
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RESULT 13
BF806978
LOCUS
DEFINITION

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ORIGIN

Pred. No.:

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SOURCE ORGANISM

REFERENCE

AUTHORS

FEATURES

Seq primer: puc 18 forward

quality sequence stop: 324.
Location/Qualifiers

/organism="Homo sapiens"
/mol\_type="mRNA"
/db\_xref="taxon:9606"

source

COMMENT

JOURNAL MEDLINE PUBMED

TITLE

ACCESSION VERSION

KEYWORDS

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VERSION
KEYWORDS
SOURCE
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AUTHORS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE100055 325 bp mRNA linear EST 13-JUN-2000 UI-R-BJ1-atm-b-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-atm-b-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          Email: bento-soares@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 93-134,
-GC_rich#Low_complexity 135-216, >(GGA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996) 97044477
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
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319 335 9565
/organism="Rattus norvegicus"
/mol type="mRNA"
/mol type="mRNA"
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/dlone="Ul-R-BJ1-atm-b-09-0-UI"
/clone="Texon: [Life Technologies)"
/clone lib="UI-R-BJ1"
/clone lib="UI-R-BJ1"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site=1: Not I; Site=2: Eco RI; The UI-R-BJ1
library is a subtracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
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                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 4156 MEBRF, Iowa City, IA 52242, USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                    221 GTATCTGAGGGCTCGGAAGTGCCCGAGAGTGAC
                                                                                              1 ValSerGluGlySerGluValProGluSerAsp
                                                                                                                                                                                                                                                                                                                                                    canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                     TAG_SEQ=None found"
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Matches:
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Mismatches:
Indels:
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                                                                    253
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EST 13-JUN-2000
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Score:

REFERENCE AUTHORS ACCESSION VERSION COMMENT BE112745 RESULT 15 SOURCE DEFINITION KEYWORDS MEDLINE PUBMED TITLE JOURNAL ORGANISM Coordinated Laboratory for Computational Genomics University of Iowa 175 Mewton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250

Fax: 319 335 9565

Fax: 319 335 9565

Fax: 319 335 9565

Small: bento-soars@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. soares Lab Clone distribution: clones will be available through soares Lab Clone distribution: clones will be available through BE112745 325 bp mRNA linear IUI-R-BJ1-avo-c-12-0-UI.sl UI-R-BJ1 Rattus norvegicus UI-R-BJ1-avo-c-12-0-UI 3', mRNA sequence. Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 93-134, >GC\_rich#Low\_complexity 135-216, >(GGA)n#Simple\_repeat Seq primer: M13 Forward Contact: Soares, MB 8889548 Genome Res. 6 (9), 791-806 (1996) discovery Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two appr Rattus Eukaryota; Metazoa; Rattus norvegicus Rattus norvegicus (Norway rat) BE112745.1 BE112745 Mammalia; Eutheria; (bases 1 to 325) Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; approaches to facilitate gene cDNA clone

FEATURES

Location/Qualifiers

/mol\_type="mRNA" /strain="Sprague-Dawley" /db\_xref="taxon:10116" organism="Rattus norvegicus"

source

/clone="UI-R-BJ1-avo-c-12-0-UI"
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/lab host="PH10B (Life Technologies)"
/clone lib="UI-R-BJ1"
/note="Vector: PT713D-Pac (Pharmacia) with a modified note="Vector: PT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ1 library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,

Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Search completed: March 13, 2004, 04:01:41 Job time: 171.319 secs US-09-976-740-21 (1-11) x BE112745 (1-325) Alignment Scores: Pred. No.: ORIGIN AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996) 5.45 54.00 100.00% 100.00% 100.00% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 325 0 0 0

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Command line parameters:

-MODEL-frame+ pln.model -DEV=xlp
-Q=/cgn2 1/USFTO spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-Q=/cgn2 1/USFTO spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-Q=/cgn2 1/USFTO spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-Q=/cgn2 1/USFTO spool_p/US0976740_cgnd_-SUDE-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWIT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09976740_cGN 1 1 9705 @runat_10032004_094548_19540 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREAUS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Perfect score:
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    March 12, 2004, 19:49:56; Search time 151.885 Seconds (without alignments) 2853.675 Million cell updates/sec
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Fgapop 6.0 , Fgapext
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Compugen Ltd
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29: em_vi:*
30: em_htg_inv:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
40: em_htg_wam:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Result No. ი იი Score Query Match Length В RR19531 AR409328 AR409328 BDX239590 BDX239590 BDX13847 BCD113847 BCD15344 BD275344 BD275344 BD27539573 BR409322 AR409337 AR409339 ACC134005 ACC134 AR374693 Sequence AR49328 Sequence AR239590 Sequence AR239590 Sequence AR239590 Sequence BD113847 Sequence BD113847 EST and e BC007384 Homo sapi AR499312 Sequence AR499317 Sequence AR499317 Sequence AR499318 Sequence AR239607 Sequence AR239607 Sequence AR239607 Sequence AR239608 Homo sapi AR409318 Sequence AR409318 Sequence AR409318 Sequence AR409319 Sequence AR199541 Sequence AR374693 Sequence AR409328 Sequence Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Homo sapi Sequence Sequence Rattus no Requence Sequence Sequence

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AR374693
AR374693.1
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, Lees, A.M., Lees, R.S., Law, S.W. and Arjona, Low density lipoprotein binding proteins a diagnosing and treating atherosclerosis patent: US 635451-A 33 12-MAR-2002;

Location/Qualifiers
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Sequence
AR199541
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1 (bases 1 to 30)
1 (bases 1 to 30)
1 Loes, A.M., Lees, R.S., Law, S.W. and Arjona
1 Low density lipoprotein binding proteins
diagnosing and treating atherosclerosis
Patent: US 6605588-A 33 12-AUG-2003;
1 Location/Qualifiers
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/mol_type="genomic DNA"
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RESULT 5
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VERSION
KEYWORDS
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Best Local Similarity:
                                                                                                            US-09-976-740-22 (1-10)
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Novel low
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Low density liprotein binding proteins and the
and treating atherosclerosis
Patent: WO 0164874-A 33 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6632923-A 33 14-OCT-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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density lipoprotein
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic I
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Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

Patent: JP 2001506983-A 13 29-MAY-2001;

BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/13

PD 29-MAY-2001

PF 26-NOV-1997 JP 1998524870

PF 26-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI

ARN M 1LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC

A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC

COTH21/00, COTK14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC

Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
FH Key Total (Acation/Qualifiers.
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Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                    1 (bases 1 to 425)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 9791 28-OCT-2003;
                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                            Sequence
AR418294
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1 (bases 1 to 30)
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BD056455
BD056455.1 GI:22602061
JP 2001506983-A/13.
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/mol_type="genomic DNA"
/db_xref="taxon:6100"
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'mol_type="genomic
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PD 15-JAN-
PF 07-AUG-
PR 05-AUG-
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C12N1/21,
PC C12N5/00
C12N15/00
CC EST a
FH Key
FT SOURC
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 425)
Edwards, J. B.D. M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 5924 15-JAN-2002;
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EST and encoded human
BD113847
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IMAGE:3677194), partial cds.
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JP 2002010789-A/5924
15-JAN-2002
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05-AUG-1999 US 60/147499
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 20, 2003 this sequence version replaced gi:13938477.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer General Canada (MGC), Cancer Genomics Office, National Cancer Genomics Office, National Cancer General Canada (MGC), Cancer Genomics Office, National Cancer G
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mol_type="mRNA"
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CDS gene JOURNAL MEDLINE PUBMED REFERENCE

TITLE

AUTHORS TITLE JOURNAL

REMARK COMMENT

in signalling and nuclear proteins. In EPH-related tyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"

/db\_xref="CDD:smart00454"

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y 1 GluAspAsj          b 679 GAGGATGA'	pAspProAspGlyPheLeuGly 			
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AUTHORS Komatsouli TITLE 49 Human S JOURNAL Patent: JF	s,G., Rosen,C.A ecreted Protein 2002539787-A 1	and Ruben, S.M. 18 26-NOV-2002;		
OMMENT OS HOMO SA PN JP 2002 PD 26.NOV- PF 16-MAR- PR 23-MAR- PR 23-MAR- FH Key	OS Homo sapiens PN UP 2002539787-A/18 PD 26-NOV-2002 PF 16-MAR-2000 JP 2000606: PR 23-MAR-1999 US 60/1.1 George komatsoulis,craig a 1 FH Key	piens 539787-A/18 539787-A/18 52002 2000 JP 2000606742 2000 JP 2000606742 1999 US 66/126054,10-DEC-19 1999 US 66/126054,10-DEC-19 100cation/Qualifiers.	199 US 6	50/169916 PI
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AR374687
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AR409322
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                                                                                                                 622 GAGGATGATGACCCCGATGGCTTCTTAGGC
Unknown.
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Sequence 16 from patent
AR374687
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Lees, A.M., Lees, R.S.,
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6605588-A 16 12-AUG-2003;
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 6632923-A 1614-CCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density liprotein binding proteins and their
and treating atherosclerosis
Patent: WO 0164874.A 16 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WO0164874.
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                                                                         Gaps:
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Indels:
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GluAspAspAspProAspGlyPheLeuGly 10

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RESULT 15
BC030129
LOCUS
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Best Local Similarity:
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TITLE
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1 (bases 1 to 1208)

1 Lees,R.M., Lees,R.S. and Arjona,A.A.

Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

AL Patent: JP 2001506983-A 7 29-MAY-2001;

PATENT FOUNDATION INC
PN JP 2001506983-A/7
PR 27-NOV-1997 JP 1998524870
PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARJONA PC A61X38/04,A61X38/17,A61X39/00,A61X48/00,A61X49/00,A61X51/08, PC C07K21/00, C07X14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC Topology: Linear;
CC Topology: Linear;
FH Key Linear;
FH Key Linear;
CC Topology: Linear;
CC T
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1470 bp mRNA linear PRI 16-Si
Homo sapiens hypothetical protein BC007384, mKNA (cDNA clone
IMAGE:3943601), partial cds.
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1 (bases 1 to 1470)
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/mol_type="genomic DNA"
/db_xref="taxon:6100"
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1. .1208
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Indels:
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FEATURES

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source
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Series: IRAL Plate: 15 Row: m Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction.
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Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA semences
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Brinkley, C., Brooks, S.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Sequencing Maryland;
Gaithersburg, Maryland;
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On Aug 19, 2003 this sequence version replaced
Contact: MGC help desk
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Tissue Procurement: DCTD/DTP
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/codon_start=3
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/protein_id="AAH30129.1"
/db_xref="GI:33871479"
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/db_x
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
/lab_host="DH10B-R"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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REMARK COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL MEDLINE TITLE

PUBMED

Search completed: March 13, 2004, 00:35:27 Job time : 152.885 secs	Qy 1 GluAspA:         Db 858 GAGGATG	US-09-976-740-22 (1-10) x BC030129 (1-1470)	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	misc_feature
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3, 2004, 00:	GluAspAspAspProAspGlyPheLeuGly 10	BC030129 (1	0.397 58.00 100.00% 100.00% 100.00%	/gene="LOC90378" /gene="LOC90378" in signalling and nuclear tyrosine kinases, appears signal transduction via t proteins to a conserved t proteins to a conserved t In many cases mediates ho /db_xref="CDD:smart00454"
LeuGly 10         TTAGGC 887	1470)	Length: Matches: Conservative: Mismatches: Indels: Gaps:	/gene="LOC90378" /gene="LOC90378" /note="SAM; Region: Sterile alpha motif. /note="SAM; Region: Sterile alpha motif. in signalling and nuclear proteins. In E tyrosine kinases, appears to mediate cel signal transduction via the binding of S signal transduction via the binding of S proteins to a conserved tyrosine that is In many cases mediates homodimerisation" /db_xref="CDD:smart00454"	
			1470 10 0	/gene="LOC90378" /gene="LOC90378" /note="SAM; Region: Sterile alpha motif. Widespread domain in signalling and nuclear proteins. In EPH-related tyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"

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Result
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-Q=/Ggn2_1/USPTO_Spool_p/US09978740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N Geneseq_29Jan04 -QFMT-fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -FIRE MAX=100 -THR MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -CUTTMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
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-NUSER-US09976740_@CGN 1 11596 @runat 10032004 094547 19532 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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New isolated low density lipoprotein binding polypeptide for treating diagnosing {\tt and/or} identifying therapeutic agents for atherosclerosis.
                                                                             WPI; 2001-565505/63.
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## ALIGNMENTS

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02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
                                                                                                                                                                   28-FEB-2001; 2001WO-US006356
                                                                                                                                                                                                                                                                                                                                                               Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Low density lipoprotein binding protein (LBP) polynucleotide
                                              BOSTON HEART FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Law SW,
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Arjona
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Disclosure; Page 9; 143pp; English.
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The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPs) of the invention (see AAB82797-820). LBPs are capable of binding to native and methylated low density lipoproteins (LDLs). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions

Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 U; 0 Other;

US-09-976-740-22 (1-10) x AAH26505 (1-30)	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
х ААН26505	0.0025 58.00 100.00% 100.00%
(1-30)	Length: Matches: Conservative: Mismatches: Indels: Gaps:
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GAGGATGACCCCCATGGCTTCTTAGGC 30
              GluAspAspAspProAspGlyPheLeuGly 10
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AAC59574 standard; cDNA; 1134 BP

26-JAN-2001 (first entry)

Human secreted protein gene 9 SEQ ID NO:19.,

RESULT 2
AAC59574/c
ID AAC595
XX AAC595
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XX Human;
XX Human;
XW Human;
XW Gastroo
KW Gastroo
KW Gastroo
KW Gastroo
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KW Food a
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Homo sapiens.

WO200056883-A1

28-SEP-2000

16-MAR-2000; 2000WO-US006822.

10-DEC-1999; 23-MAR-1999; 99US-0126054P 99US-0169916P

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM, Komatsoulis 9

P-PSDB; 2000-587666/55 AAB34307.

Human secreted proteins and gene sequences encoding them, useful for detecting, preventing, and treating disorders such as cancer, neurological disorders and immune system disorders.

Claim 1; Page 344; 429pp; English

invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial. The polynucleotides can be used for the detection of various disorders such as cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The secreted proteins can be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wound healing, and infectious diseases. The proteins can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC59557 to AAC59565 and AAB34298 represent sequences used in the exemplification of the present invention The polynucleotide sequences given in AAC59566 to AAC59614 encode the human secreted proteins given in AAB3429 to AAB34347. AAB34348 to AAB343437 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present

Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

US-09-976-740-22 (1-10) x AAC59574 (1-1134)	Alignment Scores: pred. No.: Score: Percent Similarity: Pest Local Similarity: Query Match: DB:
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GAGGATGACCCCGATGGCTTCTTAGGC	1 GluAspAspAspProAspGlyPheLeuGly 10
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RESULT 3

AAV32838 AAV32838 standard; cDNA; 1208 BP

AAV32838;

09-NOV-1998 (first entry)

Human low density lipoprotein binding protein LBP-2 cDNA

Low density lipoprotein binding protein; LDL binding protein 2; LBP-2; receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.

Homo sapiens

WO9823282-A1.		misc_feature	ł	misc_feature		1	misc_feature			misc_feature		CDS	Key	
	/*tag= e /note= "Claim 15"	651	/*tag= d /note= "Claim 14"	6799	/note= "Claim 12"	/*tag= b	2266	/note= "Claim 13"	/*tag= c	2299	/*tag= a	1654	Location/Qualifiers	

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26-NOV-1997; 97WO-US021857

27-NOV-1996; 03-JUN-1997;

96US-0031930P. 97US-0048547P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-2 (see AAW49041). It was isolated by screening human liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA clones (see AAW32834-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerosic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP
                                                                                                                                                                                                                            Human low density lipoprotein binding protein 2 (LBP-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1208 BP; 252 A; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig 16; 47pp; English
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                                                                                                                                                                                                                                                          12-NOV-2001
                                                                                                                                                                                 Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
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WO200164874-A2

21-SEP-2000

Homo sapiens.

WO200055173-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were isolated from human foetal brain, liver and aorta cDNA libraries using rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in AH26499, and a genomic DNA sequence is given in AH26495. LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions,
                                                                                                                                                                   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human breast and ovarian cancer associated antigen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF21860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising an LB
are also claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF21860 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match:
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2000US-00616289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 G;
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                             anticonvulsant;
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neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias, wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases
                                                                                                                                                                                                                                                                                                                     associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 670-671; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.: US-09-976-740-22 (1-10)  $\vdash$ GluAspAspAspProAspGlyPheLeuGly 0.159 58.00 100.00% 100.00% 100.00% x AAF21860 (1-1336) Length:
Matches:
Conservative:
Mismatches:
Indels: 10 1336 10 0 0 0

Sequence 1336 BP; 318 A; 396 C;

348

G; 270

T; 0 U; 4 Other,

В Ś 694 GAGGATGATGACCCCGATGGCTTCTTAGGC 723

AAH26499 standard; DNA; 1614 AAH26499;

₽P

12-NOV-2001 (first entry)

Human low density lipoprotein binding protein 2 (LBP-2) DNA.

RESULT 6
AAH26499
ID AAH2
XX AAH2
AC AAH2
AC LOW
DT 12-N
XX
DE Huma
XX
LOW
KW LOW
KW Athe
KW ds.
XX
Homc
XX
Homc
XX
W ds.
XX
YX
WO2( Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

Homo sapiens

WO200164874-A2

02-MAR-2000; 14-JUL-2000; 07-SEP-2001 P-PSDB; Lees AM, 28-FEB-2001; 2001WO-US006356 (BOST-) BOSTON HEART FOUND INC 2001-565505/63. DB; AAB82806. Lees RS, 2000US-00517849 2000US-00616289 Law SW, Arjona AA;

New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.

Claim 7; Fig 7A; 143pp; English.

The present sequence is that of the coding region of the human gene (See Cl also AAH26494) encoding novel human low density lipoprotein binding CC protein 2 (LEP-2, see AAB2806). The gene was isolated from a genomic DNA cl library using LEP-2 cDNA as probe. The LEP-2 protein predicted from the compresent sequence differs from that predicted from a cDNA clone (see CC Present sequence differs from that predicted from a cDNA clone (see CC Laimed polymucleotides of truncation). LEP-2 nucleic acids at its N-cc terminus (the cDNA is a 5' truncation). LEP-2 nucleic acids are among CC claimed polymucleotides of the invention that encode novel polypeptides (CC apable of binding to native and methylated LDL. Also claimed are isolated LEP polypeptides, and biologically active fragments and compositions of them, as well as expression vectors, cells and methods for producing the LEPs. Methods of determining if an animal is at risk for atherosclerosis, methods for treating an agent for use in treating catherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LEP are claimed. Pharmaceutical compositions, care also claimed

Sequence 1614 BP; 243 A; 638 ი, 564 G; 169 Ή. 0 U; 0 Other,

S US-09-976-740-22 (1-10) x AAH26499 Query Match: DB: Percent Similarity: Best Local Similarity: Pred. No.: Alignment Scores: Score <u>د ـ</u>ـــ GluAspAspAspProAspGlyPheLeuGly 0.196 58.00 100.00% 100.00% (1-1614)Length: Matches: Conservative: Gaps: Mismatches: Indels: 10 1614 10 0 0

밁 1585 GAGGATGATGACCCCGATGGCTTCTTAGGC 1614

AAH26495 RESULT

AAH26495 standard; DNA; 12425

AAH26495;

12-NOV-2001 (first entry)

Human low density lipoprotein binding protein 2 (LBP-2) gene.

Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

Homo sapiens.

2832. .5153 Location/Qualifiers

/\*tag= a
/note= "includes introns"

exon

intron

.4207

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                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                              US-09-976-740-22 (1-10)
                                                                                                                                      Alignment Scores:
                                                                                                                                                                                The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for revaluating an agent for use in treating atherosclerosis, and methods for revaluating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
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No.:
                                                                                                                                                                                                                                                                                                                                                                                    New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000; 2000US-00616289.
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                                                                                                                                                             Sequence 12425
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DB; AAB82806.
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GAGGATGATGACCCCGATGCCTTCTTAGGC 5150
                GluAspAspAspProAspGlyPheLeuGly 10
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                                                                                                                                                             BP; 2563 A;
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                                                                 Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                      Conservative:
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U;
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RESULT 8

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US-09-976-740-22 (1-10) x AAH26489 (1-1362)

GluAspAspAspProAspGlyPheLeuGly 10 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696

RESULT 9

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Percent Similarity:
Best Local Similarity:
                                                                         Alignment
Pred. No.:
              Query Match:
                                                                                                                                                        The present sequence is that of cDNA encoding a portion (see AAB82799) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAR26500. The invention provides claimed polymolectides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypoptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for revaluating an agent for use compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions. are also claimed
                                                                                                                     Sequence 1362 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-565505/63.
P-PSDB; AAB82799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000; 2000US-00517849
14-JUL-2000; 2000US-00616289
                                                                                                                                                  compositions, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 12; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rabbit low
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOST-) BOSTON HEART FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lees RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              density lipoprotein binding protein 2 (LBP-2) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L. .955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                     259 A; 421 C; 419
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54.00
100.00%
90.00%
93.10%
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              Conservative: Mismatches: Indels:
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Matches:
Gaps:
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AAH26490

AAH26490

III AAH22

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AAC AAH2

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AAC AAH2

AAC AAH2

XX

AAC AAH2

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AAC AAH2

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AAC AAC AAC

AAC AAC

CCC AAC

CCC AAC

CCC AAC

CCC AAC

CCC AAC

AAC

CCC CAC

CC Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine; WO200164874-A2 Oryctolagus cuniculus. Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA 12-NOV-2001 AAH26490; AAH26490 standard; cDNA; 1422 BP (first entry /\*tag= a /partial Location/Qualifiers 1. .955

07-SEP-2001.

28-FEB-2001; 2001WO-US006356

02-MAR-2000; 2000US-00517849. 14-JUL-2000; 2000US-00616289.

(BOST-)

Lees AM, Law SW, Arjona AA;

P-PSDB; WPI; 2001-565505/63

diagnosing New isolated low

Example

CC The present sequence is that of cDNA encoding a portion (see AAB82800) of movel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA cc was isolated following screening of a rabbit cDNA library for clones cenciding LBPs that bound to both native low density lipoprotein (LDL) and cc methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in cc AAH26491. The invention provides claimed polymuclectides encoding novel cc polypeptides which are capable of binding to native and methylated LDL, ct he isolated polypeptides, termed LBPs, and biologically active fragments cand analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an cc animal is at risk for atherosclerosis, methods for evaluating an agent cf or use in treating atherosclerosis, methods for treating a cell compositions comprising an LBP polypeptide or nucleic acid, and vaccine cc compositions, are also claimed

밁 Ś Score: US-09-976-740-22 Query Match: DB: Percent Similarity: Best Local Similarity: Pred. Alignment Scores: No.: 727 GluAspAspAspProAspGlyPheLeuGly (1-10)0.986 54.00 100.00% 90.00% 93.10% 5 x AAH26490 (1-1422)Mismatches: Indels: Gaps: Matches: Conservative: 756 10 1422 0001

Sequence 1422 BP; 265 A; 447 C; 442 2; Fig 13; 143pp; English. AAB82800 BOSTON HEART FOUND INC Lees RS, ed low density lipoprotein binding polypeptide for treating and/or identifying therapeutic agents for atherosclerosis. G; 268 T; 0 U; 0 Other;

RESULT 10 AAV32835 Key Low density lipoprotein binding protein; LDL binding protein receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccin 09-NOV-1998 AAV32835; AAV32835 standard; cDNA; 1617 BP WO9823282-A1 misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature Oryctolagus cuniculus. Rabbit low density lipoprotein binding protein LBP-2 (first entry /\*tag= g /note= "Claim 631. .660 /\*tag= a 156. .1617 361. .396 /\*tag= 313. .360 313. .396 /\*tag= d /note= "Cla /\*tag= note= "Claim /\*tag= b /note= "Claim Location/Qualifiers note= "Claim 'note= "Claim \*tag= 96. .1617 .660 .954 "Claim 21" laim ω ຫຼ 181 19" οĎ

CDNA

vaccine;

LBP-2;

04-JUN-1998.

26-NOV-1997; 97WO-US021857

27-NOV-1996; 03-JUN-1997; 96US-0031930P. 97US-0048547P.

(BOST-) BOSTON HEART FOUND INC.

Lees AM, Lees RS, Law SW, Arjona

P-PSDB; 1998-322455/28. DB; AAW49038.

subjects at risk. Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying

Claim 4; Fig 11; 47pp; English

This cDNA clone codes for novel rabbit low density lipoprotein (LDL) binding protein LBP-2 (see AAW49038). It was isolated by functional screening of a cDNA library, produced from balloon-deendothelialised healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to bind both native and methyl LDL. cDNA clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in an aspect of LBP metabolism or structure is diagnostic a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for greenatal screening); methods for treating atherosclerosis (including g (including gene of.

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and

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RESULT 11
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Best Local Similarity:
The present sequence is that of cDNA encoding a portion (see AAB82798) c novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) armethyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated
                                                                                                                                                                    New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000;
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2000US-00616289.
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                                                                                                   New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000;
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DB; AAB82807.
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The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragmer

methylated LDL, y active fragmen

encoding methyl

WPI; 2003-110410/10

homologous

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RESULT 13
ABX57356
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Rameaka JG,
Garcia CA,
Hurban P;
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genetic modif
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                                                                                                         (GARC,
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                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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                                                                                                                                                                                                                                       GORLACH J.
                                                                                                                                      WOESSNER J P.
                                                                                                                                                         PAGE A.
MATHEW A V.
                                                                                                                                                                     PAGE
                                                                                                                                                                            RAMEAKA J G
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                                                                                                                                                                                                                   HAMILTON C M
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Page A, M
Kricker M,
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                               JP,
                    JP, Haas WD;
Hoffman N;
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The invention relates to Arabidopsis thaliana nucleic acid sequences. The CC DNA sequences and the polypeptides they encode are useful for identifying chomologous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional regions of the protein, in diagnosis, for studying associated regions of the protein, in diagnosis, for studying associated plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of converted transgenic organisms, such as plant colls and plants. Transgenic plants colls in plants and to create genetically modified and transgenic organisms, such as plant cells and plants. Transgenic plants collegance in plants, screening biologically active agents, such as collegance and stress converted to the print of the sequence data for this patent converted and transport of the print of specification but was obtained in the converted production of the print of the sequence data for this patent converted to the print of the sequence of the sequence of the sequence of the print of the print of the print of the sequence of 
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or related genes, and to create genetically modified
organisms, such as plant cells and plants.
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ed and transgenic
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Sequence 539

BP;

130 A; 151 C; 100 G; 158 T; 0

U; 0 Other;

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Best Local Similarit
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                                                                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                              ABZ14503
                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 2306
WPI; 2002-304127/34
                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                Arabidopsis thaliana;
                                                                                                                                                                                                   21-JAN-2003
                                                                                                                                                                                                                    ABZ14501;
                                                                                                                                                                                                                                     ABZ14501
                                                         24-AUG-2000; 2000US-0227866P
26-JAN-2001; 2001US-0264647P
22-JUN-2001; 2001US-0300111P
                Harper JF,
                                 (SCRI )
                                                                                              24-AUG-2001;
                                                                                                              28-FEB-2002
                                                                                                                                WO200216655-A2
                                                                                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                      1 GluAspAspAspProAspGlyPheLeuGly 10
                                 SCRIPPS RES INST
SYNGENTA PARTICII
                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                       GAGGATCGTGATCCTCAAGGCTTCCTTGGA
                Kreps J,
                                                                                              2001WO-US026685
                                                                                                                                                                                                   (first entry)
                                  PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                  27.5
44.00
80.00%
80.00%
75.86%
                                                                                                                                                                                                                                     DNA; 2838
                Wang
                                                                                                                                                                 plant; gene;
                  ×
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                                                                                                                                                                                                                                                                                                         (1-539)
                  Zhu
                                    AG
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                     Indels:
                   H
                                                                                                                                                                  stress;
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Claim 144; SEQ ID NO 2306; 577pp + Sequence Listing; English

producing

Identifying a stress c producing plants with

condition to which a plant cell has been exposed and nincreased tolerance to these abiotic stresses.

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RESULT 15
ADA68111
ID ADA68
XX ADA68
AC ADA68
AC ADA68
AC APAB1
AC
                                                                                                                                                                                                                                                                                     Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting
The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-175290/17.
                                                                                                                                                                                                                                                      expression.
                                                                                                                                             SEQ ID NO 374; 899pp; English.
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office Sequence 2838 BP; 784 A; 600 C; 703 G; 751 .. '-0 U; 0 Other;

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                                                                                                                                                       US-09-976-740-22 (1-10) x ABZ14501 (1-2838)
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Best Local Similarity:
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                                                                                                                                                                                                                          Score:
Arabidopsis thaliana gene,
                      20-NOV-2003
                                                                 ADA68111 standard; DNA; 2838
                                                                                                              352 GAGGATCGTGATCCTCAAGGCTTCCTTGGA 381
                                                                                                                                  GluAspAspAspProAspGlyPheLeuGly 10
                     (first entry)
                                                                                                                                                                                       169
44.00
80.00%
80.00%
75.86%
 SEQ ID 374.
                                                                 ВP
                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                              2838
0
0
2
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Plant; bacterial infection; fungal infection; viral infection; gg

Arabidopsis thaliana

WO2003000898-A1

22-JUN-2001; 2001WO-IB001105

22-JUN-2001; 2001WO-IB001105

(SYGN) SYNGENTA PARTICIPATIONS ĀĞ.

Chang H, Katagiri Chen W, F, Quan Cooper B, S, Tao Y, Glazebrook J, (Whitham S, Xie Goff SA, le Z, Zhu Hou Zou

r response to a plant ting plant to

> S Percent Similarity: Best Local Similari 88888888**%**& 용 US-09-976-740-22 Query Match: Alignment Scores: comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to Sequence 2838 BP; illustrate the invention. N 0 : 352 Similarity: GAGGATCGTGATCCTCAAGGCTTCCTTGGA GluAspAspAspProAspGlyPheLeuGly (1-10)784 A; 600 C; 169 44.00 80.00% 80.00% 75.86% x ADA68111 (1-2838)703 G; Gaps: Conservative: Mismatches: Indels: 751 381 Η, 0 U; 0 Other; 0 0 2 0 8 28 3 8

Search completed: March 12, Job time : 21.8507 secs 2004, 21:08:47

(4) (4) 

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-DB=1ssued_patents_NA -QFMT=fastap_-SUFFIX=rni -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740_@CGN 11 _235 eyrunat 10032004_094549_19564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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    US-08-979-608A-33

US-09-517-849-33

US-09-616-289-33

US-09-621-976-9791

US-08-979-608A-16

US-09-517-849-16

US-09-616-289-16

US-09-616-289-45

US-09-616-289-45

US-09-616-289-50

US-09-616-289-12

US-09-617-849-12
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Sequence 33, Appl
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Sequence 45, Appl
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Sequence 12, Appl
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MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-NO. 6355451-1997

PRIOR APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/048,547

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NUMBER: WIS 60/031,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
  NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08979608A
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US-09-614-912-171
US-09-614-912-171
US-09-614-912-171
US-09-614-914-172-17
US-09-614-614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Appl Sequence 13, Appl Sequence 11, Appl Sequence 111, Appl Sequence 171, App Sequence 171, Appl Sequence 171, Appl Sequence 70, Appl Sequence 77, Appl Sequence 78, Appl Sequence 79, Appl Sequence 173, Appl Sequence 173, Appl Sequence 173, Appl Sequence 173, Appl Sequence 174, Appl Sequence 102, Appl Sequence 103, Appl Sequence 104, Appl Sequence 104, Appl Sequence 106, Appl Sequence 107, Appl Sequence 107, Appl Sequence 108, Ap
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Seguence
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NAME/KEY: Coding Sequence;
LOCATION: 1...30
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-979-608A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPRONE: 617/542-5070
TELEPRA: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                  TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lees, Robert S.

Law, Simon W.
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING AFHEROSCLEROSIS
                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Max-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M.
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 Franklin Street
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                    NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09517849
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Matches:
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Indels:
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CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR EILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASCESC for Windows Version 4.0
TYPE: DNA
CROANTEN. UND CONTROL OF THE PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
LENGTH: 30
TYPE: DNA
CROANTEN. UND CONTROL OF THE PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
I NUMBER OF SEQ ID NOS: 53
LENGTH: 30
TYPE: DNA
CROANTEN. UND CONTROL OF THE PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
I NUMBER OF SEQ ID NOS: 53
I LENGTH: 30
TYPE: DNA
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                     RESULT 4
US-09-621-976-9791
                                                                                                                                                                                                                                            US-09-976-740-22 (1-10) x US-09-616-289-33 (1-30)
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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Sequence 9791, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Rober
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 33:
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No. 6632923
No. TMATIO
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LOCATION:
                                                                                                                                                                GAGGATGATGACCCCGATGGCTTCTTAGGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Matches:
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COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PASSESSO for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
RAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
RELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-979-608A-16
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Best Local Similarity:
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054APR2

FILE REFERENCE: GENSET.054APR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                    SEQUENCE CHARACTERISTICS:
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LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
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Robert S.
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Matches:
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Indels:
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; NAME/KEY: Coding Sequence;
; LOCATION: 1...651
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16
                 Alignment Scores:
Pred. No.:
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Best Local Similarity:
Query Match:
                                                                        US-09-517-849-16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                        TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY_AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FASCUSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                       SEQUENCE DESCRIPTION:
                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M.
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                                                                                                                                                                             LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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                                                                                                                                NAME/KEY:
                                                                                                                                                                 TOPOLOGY: linear
                                                                                                           LOCATION:
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                                                                                           SEQ ID NO:
Length:
Matches:
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Indels:
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Best Local Similarity:
                                                                                                                                                                                            ; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert

; APPLICANT: Law, Simon W

; APPLICANT: Arjona, Anib
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Best Local Similarity:
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-616-289-16
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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/09616289
Patent No. 6632923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-616-289-45
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APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: POTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
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SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: APPLICACION OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Law, Simon W.
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Law, Simon W.
                                                                                                                                                                                                                                                                               Robert S.
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Percent Similarity:
Best Local Similarity:
Query Match:
                                    Percent Similarity:
Best Local Similarity:
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Query Match:
DB:
                                                                                                 Alignment Scores: Pred. No.:
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PRIOR FILING DATE: 2000-03-02
PRIOR PEPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
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PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR PILING DATE: 2000-03-02

PRIOR PPLICATION NUMBER: US 08/979,608

PRIOR PILING DATE: 1997-11-26

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1997-06-03

PRIOR PILING DATE: 1997-06-03

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PRIOR PILING DATE: 1997-06-03

PRIOR PILING DATE: 1997-06-03
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SEQ ID NO 50
LENGTH: 12425
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LENGTH: 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
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                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
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                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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COMPUTER: IBM COMPACTIVE
COMPUTER: IBM COMPACTIVE
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547

FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996
AFTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION
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Best Local Similarity:
Query Match:
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US-08-979-608A-12
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  RESULT 11
                                                                                                                                                                    US-09-976-740-22 (1-10) x US-08-979-608A-12 (1-1362)
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Patent No. 635451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                             GluAspAspAspProAspGlyPheLeuGly 10
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STATE: MA
                                                        GAGGACGATGACCCGGAAGGCTTCCTGGGA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Sequence LOCATION: 1...696
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STRANDEDNESS: single
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93.10%
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Matches:
Conservative:
Mismatches:
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Gaps:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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PILING DATE: 26.NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                       Sequence 12, Application US/09616289 Patent No. 6632923
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence LOCATION: 1...696 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lees, Ann M.
Lees, Robert S.
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STATE: MA
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54.00
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Matches:
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Indels:
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1362 9

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US-09-517-849-12
                                                                                                                                      COMPUTER: IBM Compatible
operating SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
10797-003001
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US-09-9/6-/40-22.Thi
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(696)
US-09-616-289-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FITTLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR PRIOR DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PRIOR DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-976-740-22 (1-10) x US-09-616-289-12 (1-1362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08979608A Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                      APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              667 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GluAspAspAspProAspGlyPheLeuGly 10
                      APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UTN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lees, Ann M.
Lees, Robert S.
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93.10%
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Indels:
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Matches:
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
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COUNTRY: U
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TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 13 US-08-979-608A-13

APPLICANT:

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Pred. No.: Alignment Scores:

SEQ ID NO 12

REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070 10797-002001 (formerly 3983/59818)

TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

TOPOLOGY: linear Coding Sequence

LOCATION: 1...756
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

100.00% 90.00% 93.10% 0.178 54.00 Length: Matches: Mismatches: Indels: Conservative:

US-09-976-740-22 (1-10) x US-08-979-608A-13 (1-1422)

RESULT 14
US-09-517-849-13
Sequence 13, Application US/09517849
Patent NO. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S. Lees, Robert Law, Simon W.

Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street CITY: Boston USA

ZIP: 02110-2804
COMPUTER READABLE FORM:
CMEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARAE: PASTSOO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849

FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION UNIMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8006
TELEPAX: 617/542-806 NAME: Myers, Louis

ATTORNEY/AGENT INFORMATION

```
WESULT 15
US-09-616-289-13
Sequence 13, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US/09/517,849
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR FILING DATE: 1900-03-02
PRIOR FILING DATE: 1900-03-02
PRIOR APPLICATION NUMBER: US/08/979,608
PRIOR APPLICATION NUMBER: US/08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/08/979,608
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1422
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEATURE: NAME/KEY: CDS
LOCATION: (1)...(756)
                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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LOCATION: 1...756
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-517-849-13
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.178
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Mismatches:
Indels:
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9
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Search completed: March 13, 2004, 04:06:29 Job time  $\cdot$  6 39045 secs

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Title:
Perfect score:
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No.
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-MODEL-frame+ p2n.model p-USC+stp
-MODEL-frame+ p2n.model p-USC+stp
-C-/Ggn2 1/USPTO.gpool p/USC+ST40/runat 10032004 094549 19588/app query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USCR=USC9976740 @CGN 1 1 712 @runat 10032004 094549 19588
-NCPU=6 -ICPU=3 -NO MMAP -LARGSQUERY -NGEG SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein -
                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    Score
                                                                                                                                                                                     Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO NEW PUB.seq:*
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Query
Match Length DB
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58
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
    A
                                                                     SUMMARIES
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7.0
  Description
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58 100.0 30 9 US-09-962-055-33 Sequence 33, Appl 58 100.0 30 13 US-10-671-242-3 Sequence 33, Appl 58 100.0 30 13 US-10-023-529-3 Sequence 33, Appl 58 100.0 30 13 US-10-023-529-3 Sequence 33, Appl 58 100.0 30 13 US-10-023-529-3 Sequence 16, Appl 58 100.0 1208 9 US-09-962-055-16 Sequence 16, Appl 58 100.0 1208 12 US-10-671-242-16 Sequence 16, Appl 58 100.0 1208 13 US-10-023-529-16 Sequence 16, Appl 58 100.0 1336 14 US-10-023-529-16 Sequence 16, Appl 58 100.0 13445 10 US-09-962-055-16 Sequence 16, Appl 58 100.0 1614 9 US-09-976-740-45 Sequence 45, Appl 58 100.0 1614 12 US-10-023-529-45 Sequence 45, Appl 58 100.0 1614 13 US-10-023-529-45 Sequence 50, Appl 58 100.0 1614 13 US-10-023-529-45 Sequence 50, Appl 59 US-09-976-740-12 Sequence 50, Appl 59 US-09-976-740-13 Sequence 50, Appl 59 US-09-976-740-13 Sequence 12, Appl 59 US-09-976-740-13 Sequence 13, Appl 59 US-09-976-740-14 Sequence 14, Appl 59 US-
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#### ALIGNMENT:

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US-09-962-055-33

(Sequence 33, Application US/09962055)

(PATENT NO. US20020052033A1)

(PATENT LEES, AND M. LEES, AND M. LAW, Simon M. Arjona, Anibal A. MITTLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN UNMBER OF SEQUENCES: 42

(CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: USA ZIP: 0210-2804

(COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COmpatible Operating SYSTEM: DOS
```

AND

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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION UNMBER: US/09/976,740

CURRENT APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: US/09/976,608

PRIOR APPLICATION NUMBER: US 60/979,608

PRIOR APPLICATION NUMBER: US 60/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-66-03

NUMBER OF SEQ ID NOS: 53

NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELEPAN: 617/542-8906
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LEAST OF NEW STATES
INFORMATION OF NEW STATES
IN
; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-976-740-33
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US-09-976-740-33
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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                                                                                                                           SEQ ID NO 33
LENGTH: 30
                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluAspAspAspProAspGlyPheLeuGly 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-10-671-242-33
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US-10-023-529-33
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Best Local Similarity:
Query Match:
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                                                                                                                                                               Sequence 33, App
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Appropriate Publication No.
APPLICANT: Arjona, Aribal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                             APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal
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                                                                                                                                                               Application US/10023529
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Mismatches:
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                             AND TREATING
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APPLICANT: AJONA, ANIBAL A.

APPLICANT: AJONA, ANIBAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHERSOSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-07-14
PRIOR APPLICATION NUMBER: US/95/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/95/17,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1907-01-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
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Best Local Similarity:
Query Match:
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  Percent Similarity:
Best Local Similarity:
                                                                               Alignment Scores
                                                                                                                       US-10-023-523-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-976-740-22 (1-10) x US-10-023-529-33 (1-30)
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CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR PPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 06/979,608

PRIOR PILING DATE: 1997-11-26

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                 SOFTWARE: F
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-10-023-523-33
Sequence 33, Application US/10023523
Publication No. US20020152485A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lees, Ann M.
APPLICANT: Lees, Rober
APPLICANT: Law, Simon
                                                                                                                                    LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
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Law, Simon W
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Length:
Matches:
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
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US-10-616-187-33
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SEQ ID NO 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
  CITY: Boston
                                                                                                                                                                                           Lees,
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US-09-962-055-16
, Sequence 16, Application US/09962055
, Patent No. US20020052033A1
, GENERAL INFORMATION:
, APPLICANT: Lees, Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR PPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/579,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
Law, Simon W.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
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                                                                                                                                       Robert S.
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1996-11-27
PRIOR PPLICATION NUMBER: US 60/048,547
PRIOR PPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Note: Low Density Lipoprotein Binding
TITLE OF INVENTION: NOTEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09976740 Publication No. US20020194633A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MYPER, LOUIS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHAN: 617/542-5066
TELEPHAN: 617/542-8066
RMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 1...651
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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Conservative:
Mismatches:
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APPLICANT: ALGM, SAINGH M.
APPLICANT: ALGMA, SAINGH M.
APPLICANT: ALGMA, SAINGH M.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-976-740-16
                                                                                                                 US-09-976-740-22 (1-10) x US-10-671-242-16 (1-1208)
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SEQ ID NO 16
LENGTH: 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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622 GAGGATGATGACCCCGATGGCTTCTTAGGC 651
                                                       1 GluaspaspasperoaspGlyPheLeuGly 10
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Matches:
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Matches:
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Indels:
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Mon Mar 15 09:28:15 2004

RESULT 10 US-10-023-529-16

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Sequence 16, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: APPLICATION STATESCOSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT APPLICATION NUMBER: US/16,289
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-523-16
, Sequence 16, Application US/10023523
, Publication No. US20020152485A1
, GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-529-16
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEC ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
                                                                                                                                                                                                                                            APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lees, Ann M.
APPLICANT: Lees, Rober
APPLICANT: Law, Simon
APPLICANT: Arjona, Ani
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ORGANISM: Homo sapiens
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APPLICANT: AJORA, ANIDATA

TITLE OF INVENTION: NOVEL LOW DENSITY LIPODROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/616,187

CURRENT FILING DATE: 2003-07-09

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-26

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/046,547
                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (1)...(651)
US-10-023-523-16
                                                                                                                                                                                            Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(651)
US-10-616-187-16
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Best Local Similarity:
           US-09-976-740-22 (1-10) x US-10-616-187-16 (1-1208)
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SEQ ID NO 16
LENGTH: 1208
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Publication No. US20040013668A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 16
LENGTH: 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 53
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ORGANISM: Homo sapiens
FEATURE:
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Conservative:
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Matches:
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Alignment Scores:

Pred. No.:

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RESULT 13 US-10-102-806-247 CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846 Sequence 247, Application US/10102806
publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PIC1 Application US/10102806 5. US20030054421A1

SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 247 LENGTH: 1336

FEATURE: misc\_feature
NAME/KEY: misc\_feature
LOCATION: (26)
OTHER INFORMATION: n equals a,t,9, ORGANISM: Homo sapiens

; NAME/KBY: misc\_feature ; IOCATION: (1336) ; OTHER INFORMATION: n equals a,t,g, US-10-102-806-247

Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-09-976-740-22 (1-10) x US-10-102-806-247 (1-1336) Score Alignment Scores: Pred. No.: 100.00% 100.00% 100.00% 0.0615 Conservative: Mismatches: Indels: Length: Matches: 1336 10 0 0

밁 Ś 694 GAGGATGACCCCGATGGCTTCTTAGGC 723 1 GluAspAspAspProAspGlyPheLeuGly 10

RESULT 14 US-09-945-527-6 Sequence 6, Application US/09945527 Publication No. US20030055588A1 GENERAL INFORMATION:

APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20030055588A1el Nucleic Acid Molecules Encoding
TITLE OF INVENTION: Nucleic Acid and Protein Homologs
FILE REFERENCE: 35800/237985
CURRENT APPLICATION NUMBER: US/09/945,527
CURRENT FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6 ENGTH: 1445

Score: Percent Similarity: Pred. No.: Alignment Scores: 0.0664 58.00 100.00%

; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-945-527-6

Matches: Conservative:

APPLICATION ATIONAL TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US/616,289

PRIOR FILING DATE: 1907-07-14

PRIOR APPLICATION NUMBER: US/69/99,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US/60/031,930

PRIOR APPLICATION NUMBER: US/60/031,930

PRIOR PRIOR DATE: 1997-06-03

NUMBER: US/60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

NUMBER OF SEQ ID NOS: 53 Ş RESULT 15 US-09-976-740-45 Ş Percent Similarity:
Best Local Similarity:
Query Match: Alignment Scores: Pred. No.: ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)...(1614) US-09-976-740-45 맑 US-09-976-740-22 (1-10) x US-09-945-527-6 (1-1445) Best Local Similarity: 100.00% Query Match: 100.00% US-09-976-740-22 (1-10) x US-09-976-740-45 (1-1614) Score: ; SEQ ID NO 45 ; LENGTH: 1614 ; TYPE: DNA Sequence 45, Appublication No. GENERAL INFORMATION: APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W. SOFTWARE: FastSEQ for Windows Version 4.0 ORGANISM: Homo sapiens 807 GAGGATGACCCCGATGGCTTCTTAGGC 836 1 GluAspAspAspProAspGlyPheLeuGly 10 1 GluaspaspaspProAspGlyPheLeuGly 10 Application US/09976740 o. US20020194633A1 0.0741 58.00 100.00% 100.00% Length:
Matches:
Conservative:
Mismatches:
Indels: Mismatches: Indels: 1614 10 0 0 000 AND TREATING

Search completed: March 13, 2004, 04:26:15 Job time: 15.4676 secs

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1585 GAGGATGATGACCCCGATGGCTTCTTAGGC 1614

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Command line parameters:

-MODEL-frame, p2n.model -DEV=xlp
-MODEL-frame, p2n.model -DEV=xlp
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MAYRIX=blosun62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN 1 1 10232 @runat 10032004 094548 19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORESO - WAIT -DSPBLOCKE100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 s
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Ygapop 10.0 , 1
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     27513289 seqs, 14931090276 residues
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Copyright (c) 1993 - 2004 Compugen Ltd
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gb_est1: *
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# 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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#### ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AA481593/c	RESULT 1
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 313)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (human)	EST.	AA481593.1 GI:2211145	AA481593	mRNA sequence.	aa35e06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815266 5',	AA481593 313 bp mRNA linear EST 14-AUG-1997		

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RESULT 2
D80440/c
LOCUS
DEFINITION
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                          252 GAGGATGATGACCCCGATGGCTTCTTAGGC 223
                                                                                                                                                                                                     361 bp mRNA linear EST 09-FEB-1996
HJM074C06A Human fetal brain (TFujiwara) Homo sapiens cDNA clone
GEN-074C06 3', mRNA sequence.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                        Homo sapiens (human)
                                                                                                                                                                               D80440
D80440.1 GI:1178317
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.S. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Louis M. Staudt, M.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:815266"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
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Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Mithe,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal,C., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,B., Hinkle,P.S.Jr., Glodek,A., Gnehm,C.L., Hanna,M.C., Marwaros,S.M., Merrick,J.M., Kelley,J.C., Liu,L.-I., Marwaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Peng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Peng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Kozak,D.L., Kunsch,C., Ming,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 8 million nucleotides of cDNA sequence
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463-10 kagasuno Kawauchi-cho,
Tel: 0886-65-2888
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA311602
EST182332 Jurkat T-cells
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Unpublished (1995)
Contact: Tsutomu Fujiwara
                                                                   Contact: Kerlavage, AR
                                                                                               Other_ESTs: THC122721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VI Homo sapiens cDNA 5' end,
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DB:
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Tanakk,T., Ohgi,T. and Yano,J.
cDNA microarray analysis of altered gene expression in
Ara-C-treated leukemia cells
                                                                                                                                                                                                Nippon Shinyaku Co. Ltd.
Sakura 3-14-1, Tsukuba, Ibaraki
Tel: 81-29-850-6217
Fax: 81-29-850-6217
                                                                                                                                                                                                                                             Contact: Kazuchika Takagaki
Research Laboratories
Nippon Shinyaku Co. Ltd.
                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 309 22831100
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone LEU4076_8_D5, mRNA sequence.
BP432333
BP432333.1 GI:34555032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP432333 leukemia cell normalized cDNA library Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bmail: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 3018699056
Fax: 3018699423
Email: arkerlay
                                                                                                                                                                   k.takagaki@nippon-shinyaku.co.jp.
Location/Qualifiers
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/mol type="manua"
/db xref="NTCC (inhost):158827"
/db xref="taxon:9606"
/cell type="T-lymphocyte"
/clone libe-"Jurkat T-cells VI"
/note="Vector: pBluescript SK-; S
                        /organism="Homo sapiens"
/mol type="mrNA"
/db_xref="rexxon:9606"
/clone="LEU4076_8_D5"
/cell type="leukemia cell"
/clone lib="leukemia cell normalized cDNA library"
/note="mrNA expressed in leukemia cells (mixture of CCRF-CEM, K562, HI-60, MOLT-4, or RPMI-8226)"
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Matches:
Conservative:
Mismatches:
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Gaps:
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KEYWORDS
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AI247702/c
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AUTHORS
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CB802479
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Alignment

Scores:

ORGANISM

sapiens (human) sapiens

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US-09-976-740-22 (1-10)
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DB:
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                                          AI247702 427 bp mRNA linear qh60h02.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo clone IMAGE:1849107 3' similar to TR:P78365 P78365
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HOMOLOG. ;, mRNA sequence.
AI247702
AI247702.1 GI:3843099
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Rattus norvegicus
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amgen EST Program
Amgen Rat EST Program
Unpublished (2003)
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                                                                                                                                                      GluAspAspAspProAspGlyPheLeuGly
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                                                                                                                                                                                                                                                                                                                                                         /tissue_type="prostate tissue"
/clone_Tib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sall;
prostate normalized double selected pofraction > 1 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                          EST 01-DEC-1998
sapiens cDNA
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BQ317482
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AUTHORS
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BQ317482.1
                                                                                                  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Eriones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Grunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 427)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                               Brunstein, A., deOliveira, P.S., Bucher, P., Jongenee O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.,
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                      BQ317482
RC1-CT0302-040400-017-d09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 587 Std Error: 0.00
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Unpublished (1997)
                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                             sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluAspAspAspProAspGlyPheLeuGly 10
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Location/Qualifiers
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1849107"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento Soares and M.Fatima Bonaldo."
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                 Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                      (human)
                                                                                                                                                                                                                                                                                                                            430 bp mRNA linear
CT0302 Homo sapiens cDNA,
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Matches:
Conservative:
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI057236 436 bp mRNA linear EST 29-SEP-19:
ozl1d06.xl Soares_fetal_liver_spleen_INFLS_SI Homo sapiens cDNA
clone_IMAGE:1675019 3' similar to TR:P78365 P78365 POLYHOMEOTIC 2
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This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-CT0302-040400-017-d09&t3=2000-04-04&t4=1)

Seq.primer: puc 18 forward

Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GluAspAspAspProAspGlyPheLeuGly 10
                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infc@image.llnl.gov) for further information.

INSET Length: 593 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 351.

Location/Qualifiers
                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 436)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI057236
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/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min:library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mana and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/organism="Homo sapiens"
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VERSION
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NCI/NIMDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                          Insert Length: 685 Std Error: (Seq primer: -40UP from Gibco High quality sequence stop: 374.
                                                                                                                                                                                                    DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 685 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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AI198288.1 GI:3750894
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AI198288
AI198288
Gi61d04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1860967 3'
Similar to TR:P78365 P78365 POLYHOMEOTIC 2 HOMOLOG. ;, mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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//lab host="DH10B (ampicillin resistant)"
//clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
//clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: Jiste_2: Eco RI;
//nis is a subtracted version of the original Soares fetal
liver spleen iNFLS library. 1st strand cDNA was primed
//nis spleen iNFLS library. 1st strand cDNA was primed
//nis spleen iNFLS library. 1st strand cDNA was primed
//note="Organ: Library and Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I
//note="Organ: Library and Eco RI sites of the modified pT7T3 vector: Library constructed by Bento Soares and M.Fatima Bonaldo."
  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1860967"
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/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                       /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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US-09-976-740-22 (1-10) x AI198288 (1-454)
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1 (bases 1 to 454)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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454 bp mRNA linear EST 14-APR-1999 tm68h04.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163319 3' similar to TR:P78365 P78365 POLYHOMBOTIC 2 HOMOLOG. ;, mRNA
                                                                                                                                  Seq primer: -40UP from Gibco
High quality sequence stop: 372.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 698 Std Error: 0.00
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2163319"
                                                                                                                 . 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iow CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics University of Iowa 775 Newton Road, 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu
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Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM714074.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM714074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluAspAspAspProAspGlyPheLeuGly 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   do,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                          /organism="Homo sapiens"
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/db xref="taxon:9606"
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Choroid"
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/clone_lib="UIS-EJO"
/note="forgan: eye; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.02
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Matches:
Conservative:
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0
0
                                                                                                                                                                   (T1 phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Univeristy of Iowa
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REFERENCE AUTHORS TITLE

(bases 1 to 461) naldo, M.F., Lenno

COMMENT

Contact: Soares, MB

MEDLINE PUBMED JOURNAL

8889548

Genome Res. 6 (9), 791-806 (1996)

discovery

FEATURES

Seq primer: M13 POLYA=Yes.

ocation/Qualifiers

Genetics (www.resgen.com). Seg primer: M13 Forward

Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research

Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565

source

/clone="UI-E-EJO-ahr-h-07-0-UI"
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optic nerve, retina, Retina Foveal and Macula

Macular, RPE a

and

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(T1 phage resistant)"

Choroid"

VERSION KEYWORDS

ACCESSION

DEFINITION вм675258/с RESULT 12

Focus

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Normalization and subtraction: two approaches to facilitate gene

Lennon, G. and Soares, M.B.

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                            US-09-976-740-22 (1-10) x BM714074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                               149 GAGGATGATGACCCCGATGGCTTCTTAGGC
                                                                                       BM675258 461 bp mRNA linear EST 27 UI-E-EJO-ahr-h-07-0-UI.s1 UI-E-EJO Homo sapiens cDNA clone UI-E-EJO-ahr-h-07-0-UI 3', mRNA sequence.
                                                   BM675258.1 GI:18985156
                                                                          BM675258
Homo sapiens (human)
                                                                                                                                                                                                                                                                                GluAspAspAspProAspGlyPheLeuGly 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAACA; lens, CGATTAGCGA; eye anterior segment, AATGCGCAT; optic nerve, CCATTAACTG; retina, CCGCG; Retina Poveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                 3.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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Indels:
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                                                                                                                                                                                                                                                    178
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Score: Pred. No.:

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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
BM842690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-976-740-22 (1-10) x BM675258 (1-461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GluAspAspAspProAspGlyPheLeuGly 10
                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 68 row: F column: 06
High quality sequence stop: 464.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM842690 464 bp mRNA linear EST 06-MAR-2002 K-EST0120140 S12SNU216 Homo sapiens cDNA clone S12SNU216-68-F06 5',
                                                                                                                                                                                                                                                                                                                           Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM842690.1 GI:19199099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 464)
n,N.S., Hahm,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-B-500 is a subbracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) lB tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
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TAG_LIB=UI-E-EJ0
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Matches:
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Indels:
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ORIGIN

#### REFERENCE AUTHORS KEYWORDS SOURCE RESULT 14 BM842726 LOCUS COMMENT FEATURES Ś DEFINITION 밁 US-09-976-740-22 (1-10) x BM842690 (1-464) Query Match: DB: Percent Similarity: Best Local Similarity: Score: VERSION ACCESSION Pred. No.: Alignment Scores: TITLE JOURNAL ORGANISM source 249 GAGGATGATGACCCCGATGGCTTCTTAGGC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 464) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Che, V., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Vim, V., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 1 GluaspaspaspProaspGlyPheLeuGly 10 Email: yongsung@mail.kribb.re.kr Plate: 66 row: B column: 02 High quality sequence stop: 464. Location/Qualifiers Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Kim, Y.S. 21C Frontier Korean EST Project 2001 mRNA sequence. BM842726 464 bp mRNA linear EST 06-MAR-2002 K-EST0120184 S12SNU216 Homo sapiens cDNA clone S12SNU216-66-B02 5', Fax: +82-42-860-4409 Genome Research Center Contact: Kim YS Unpublished (2002) Homo sapiens BM842726.1 GI:19199135 BM842726 Homo sapiens (human) /tissue\_type="Lymph node" /cell\_type="Epithelial" /cell\_line="SNU-216" /lab\_host="Top10F'" /db\_xref="taxon:9606" /clone="S12SNU216-66-B02" organism="Homo sapiens" /mol\_type="mRNA" 'clone\_lib="S12SNU216" 3.1 58.00 100.00% 100.00% 100.00% Matches: Conservative: Mismatches: Indels:

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE BM840318 LOCUS Best Local Similarity: Query Match: COMMENT US-09-976-740-22 (1-10) x BM842726 (1-464) Alignment Scores: ORIGIN FEATURES RESULT 15 Percent Similarity: Score: Pred. No.: DEFINITION TITLE ORGANISM source 249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278 Email: yongsung@mail.kribb.re.kr Plate: 41 row: E column: 05 High quality sequence stop: 466. Location/Qualifiers Korea Research Institute of Bioscience & Biotechnology 52 Eceum-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 1 (bases 1 to 466)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. BM840318 466 bp mRNA linear EST 06-MAR-2002 K-EST0117357 S12SNU216 Homo sapiens cDNA clone S12SNU216-41-E05 5', Contact: Kim YS Genome Research Center Homo sapiens Homo sapiens (human) BM840318.1 GI:19196727 BM840318 mRNA sequence. Unpublished (2002) 21C Frontier Korean EST Project 2001 Kim, Y.S. GluAspAspAspProAspGlyPheLeuGly 10 /note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI; Site\_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library." /clone\_lib="S12SNU216"
/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI;
Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with /tissue\_type="Lymph node"
/cell\_type="Epithelial"
/cell\_line="SNU-216" organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" lab host="Top10F'" 3.1 58.00 100.00% 100.00% .one="S12SNU216-41-E05" Conservative: Mismatches: Indels: 10 0 0 0

bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 KNA lingse and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

ATTGIMETIC OCCEPT:			
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Score:	58.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	12	Gaps:	0
US-09-976-740-22 (1-10) x BM840318 (1-466)	x BM840318	(1-466)	
Qy 1 GluAspAspAspProAspGlyPheLeuGly 10	AspProAspGly	PheLeuGly 10	
Db 249 GAGGATGAT	GACCCCGATGGC	TTCTTAGGC 278	

Search completed: March 13, 2004, 04:01:47 Job time: 157.2 secs

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
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                                          1161
1047.5
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                                                                                                           1170
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seq length: 2000000000
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Match
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1170
1 EERVLEKEEEEDDDEDEDEE......HIKVLQQGHFEDDDPDGFLG 217
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aah26480 Rabbit lo
Aah26490 Rabbit lo
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### ALIGNMENTS

RESULT AAV328 ID AAV XX AC AA AC A	RESULT 1 AAV32838 AAV32838 standard; cDNA; 1208 BP.  XX XX AC AAV32838; AC AAV32838;  XX DT 09-NOV-1998 (first entry) XX
XH	
XE	Human low density lipoprotein binding protein LBP-2 cDNA.
Ş	binding protein 2;
ž ž	therapy
S ×	Homo sapiens.
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FH	Key Location/Qualifiers
FΤ	CDS 1654
FΤ	/*tag= a
FT	misc_feature 2299
F	/*tag= c
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и и Н Н	misc_feature 2266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-2 (see AAW49041). It was isolated by screening human liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA clones (see AAV2834-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerotic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying
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03-JUN-1997;
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                                                  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla
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                                                                                                                ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr
                                                                                                                                                                                                                                     HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr
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Conservative:
Mismatches:
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Gaps:
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The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see ALBB2803). Clones were isolated from human foetal brain, liver and aorta cDNA libraries using rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in ALH26499, and a genomic DNA sequence is given in ALH26495. LBP-2 nucleic acids are among claimed polymucleotides of the invention that encode novel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in
                                                                                                                                                                                                                                   New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                 WPI; 2001-565505/63.
                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000;
14-JUL-2000;
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2000US-00616289.
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       Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structure or metabolism of LBP comprising an LBP polypeptide care also claimed
                                                                                              AAH26499
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                                   low density lipoprotein binding protein 2 (LBP-2)
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                                                                                                                                  standard;
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                                                                                                                                                                                                                                                              TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
                                                                                                                                                                                                                                                                                                        AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are claimed. Pharmaceutical compositions or nucleic acid, and vaccine compositions,
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CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC
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The present sequence is that of the coding region of the human gene (see also AAH26494) encoding novel human low density lipoprotein binding CC protein 2 (IBB-2, see AAB2806). The gene was isolated from a genomic DNA CC library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the CC present sequence differs from that predicted from a cDNA clone (see CC AAB2803) in that it contains an additional 321 amino acids at its N-CC terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among CC claimed polymucleotides of the invention that encode novel polypeptides (capable of binding to native and methylated LDL. Also claimed are CC isolated LBP polypeptides, and biologically active fragments and CC analogues of them, as well as expression vectors, cells and methods of cproducing the LBPs. Methods of determining if for use in treating CC atherosclerosis, methods for evaluating an agent for use in treating CC atherosclerosis, and methods for treating a cell having an abnormality in CC structure or metabolism of LBP are claimed, Pharmaceutical compositions, CC are also claimed
   Sequence 1614 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Fig 7A; 143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000; 2000US-00616289
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DB; AAB82806.
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Percent Similarity: Best Local Similarity: US-09-976-740-7 (1-217) ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGGCCAGCCCCGGGCAGCGGCACC ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr CACCAGCTTAACGG HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr GATGATGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluAspGluGlu 5.72e-60 1170.00 100.00% 100.00% 100.00% x AAH26499 (1-1614) Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: CAAGGAGAGGTCAAGGAGTGGACC 1614 217 0

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sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the
                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antibleer; vulnerary; anticonvulsant; antibbacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                                                                                                                              New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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DB; AAB58957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antivier; valuerary; anticorvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune habenlytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; neurological diseases such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1336
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                  ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGl:
                                                                              LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLySIleTyrGluHisHisIleLys
                                                                                                                      GTTTTCCAAGAGCAGGAAATTGATGGCAAAT
                                                                                                                                              AlapheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal
                                                                                                                                                                                                          TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr
                                                                                                                                                                                                                                              GACGGGACCCCTTTGGCTGTCCTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGTCGAG
                                                                                                                                                                                                                                                              AspG1yThrProPheG1yCysProProG1yArgLysG1uLysProSerAspProValG1u
                                                                                                                                                                                                                                                                                                                                                                       CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTKTTGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGATGTCTCAGAGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC
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                                                                                                                                                                                 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA
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                                                                                                                                                                                                                                                                                           The present sequence is that of cDNA encoding a portion (see AAB82799) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polymucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for revaluating an agent for use in treating atherosclerosis, and methods for revaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine
                                                                                                                                                                                                                                                   Sequence 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000;
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                                                BOSTON HEART FOUND INC
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protein 3 (LBP-3) cDNA.

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336 97 276 77

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diagnosis; rabbit;

vaccine;

LBP-3; LDL; therapy;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
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GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg
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                                                                                ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu
                                                                                                                                                                                                                                         ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
                                                                                                                                                                                                                                                                                                      AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCTCT
                                                                                                                                                                                                                                                                                                                                SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer
                                                      CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG
                                                                                                                                    CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAAAGCCGGCAGAC
                                                                                                                                                                            ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
                                                                                                                                                                                                                   BP; 265 A;
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95.45%
88.64%
89.53%
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ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis

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RESULT 7
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  Percent Similarity:
                                                                              Alignment
                                                                                                                                                                                                       CC The present sequence is that of cDNA encoding a portion (see AAB82798) of convel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA CC was isolated following screening of a rabbit cDNA library for clones cencoding LBPs that bound to both native low density lipoprotein (LDL) and centryl LDL. A full-length sequence for LBP-2 is given in AAH85500. The convention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated compositions of them, as well as expression vectors, cells and methods of canalogues of them, as well as expression vectors, cells and methods of is at risk for atherosclerosis, methods for evaluating an agent for use compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions comprising an LBP polypeptide or nucleic acid, and vaccine
                                                      Pred. No.:
                                                                                                                                     Sequence 1617
                                                                                                                                                                                         compositions comprising an LBP polypeptide compositions, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-565505/63.
P-PSDB; AAB82798.
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14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit low
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/partial
/note= "includes in-frame stop codon at nucleotides
28. .30"
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8.44e-53
1047.50
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Best L Query DB:

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US-09-976-740-7 (1-217) x AAH26488 (1-1617)
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y Match:
                                                                                                                                                                 Low density lipoprotein binding atherosclerosis; antiarterioscle
                                                                                                                                                                                                                    Rabbit low density lipoprotein binding protein 2 (LBP-2)
                                                                                                                                                                                                                                                       12-NOV-2001
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                                                                                                                Oryctolagus
              WC200164874-A2
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                                                                                                                  cuniculus.
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                                             Location/Qualifiers
246. .1928
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of CDNA encoding novel rabbit low density lipoprotein binding protein 1 (LBP-2, see AABB2807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, and methods for treating an adent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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                                                                                                                                                       SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer
                                                                                                                                                                                                                                                                                             GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys
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CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAGAAGCCGGCAGAC
                ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
                                                                                       ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
                                                                                                                                                                                                      GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly
                                                                                                                                                                                                                                                                         CAGCATCACCAGCTGAATGGCGGCGAGCGCGGCCGCAGACCGCCAAGGAGCGGGCCAAG
                                                                                                                                                                                                                                                                                                                                           GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 2A; 143pp;
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P-PSDB; AAW49038.
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  density lipoprotein binding
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related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying subjects at risk.

Claim 4; Fig 11; 47pp; English

CC This cDNA clone codes for novel rabbit low density lipoprotein (LDL)
CC binding protein LBP-2 (see AAW49038). It was isolated by functional
CC screening of a cDNA library, produced from balloon-deendothelialised
CC healing rabbit abdominal aorta mRNA, for clones encoding LBPs able to
CC bind both native and methyl LDL. cDNA clones (see AAV32834-39) and
CC encoded rabbit and human LBPs (see AAW49037-42) are claimed. An
CC abnormality in an aspect of LBP metabolism or structure is diagnostic of
CC a risk for atherosclerosis. The invention provides: methods for
CC determining if an animal is at risk for atherosclerosis (e.g. for
CC grenatal screening); methods for treating atherosclerosis (including gene
CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent
CC formation of atherosclerotic plaque; and methods for treating a cell
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and
CC vaccine compositions are also provided, as well as recombinant vectors
CC and host cells used to produce recombinant LBP and gene Ģ,

Sequence 1617 BP; 290 A; 513 Ç 529 G; 285 T; 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

1.89e-52 1041.50 95.00% 88.18% 89.02%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1617 194 15 8 3

밁 S S 8.8 밁 Ś 밁 Ś 밁 Ş 밁 Ş β. S 밁 Ş ₽ US-09-976-740-7 (1-217) x AAV32835 652 118 592 532 352 178 772 158 712 138 472 412 292 98 58 39 78 21 -GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly CAGCATCACCAGCTGAATGGCGCGAGCGCGCGCGCAGACCGCCAAGGAGCGGGCCAAG GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys GACGACGACGTCTTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCG AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCCAGCGTTGAAAATCTATGAGCAC CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGACGGCTTCCCTGAG CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAAGCCGGCAGAC rcgaccaccegecteactececereceeserecettreceeececeesaagecagecere AGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCTCT (1-1617) de a da Toga con a de Toco de Toga de Carona d 893 197 177 157 137 651 117 591 97 77 47 57 41 38 351 20 831 771 713 531

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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and
                                                                                                                                                                             New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000; 2000US-00616289.
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                                                                                                                                             Example 4; Fig 23; 143pp; English
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XX Human; sec
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PM S 밁 Ş 멍 뭕 thing polynicipulies between the sequences of the polynicipulies of the polynicipulies of the polynicipulies of the polynicipulies sequences and proteins also homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed and the stample of activities include: neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial. The polynucleotides can be used for the detection of various disorders such as cancer, chromosome concertification, as chromosome markers, and for numerous other diagnostic or research purposes. The secreted proteins can be used to treat consorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, concertive disorders, wound healing, and infectious diseases. The proteins can also be used as a food additive or preservative to increase or decrease concertives. AAC59557 to AAC59565 and AAB3429s represent concertions used in the exemplification of the present invention Human; secreted protein; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial; gene therapy; detection; cancer; chromosome marker; chromosome identification; neural disorder; immune disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; preservative proliferative disorder; wound healing; infectious disease; preservative detecting, preventing, neurological disorders 23-MAR-1999; 10-DEC-1999; 26-JAN-2001 Human secreted proteins and detecting, preventing, and t 16-MAR-2000; 2000WO-US006822 28-SEP-2000 WO200056883-A1 Claim 1; Page 344; 429pp; polynucleotide sequences given in AAC59566 to AAC59614 encode 4996 5116 additive; 186 2000-587666/55. sapiens ÇĄ, secreted HUMAN isPheGluAspAspAspProAspGlyPheLeuGly TCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCC leArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGlyH AMATTGATGGCAMATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCA Ruben (first GENOME protein 99US-0126054P 99US-0169916P SM, CDNA; entry) SCI INC Komatsoulis gene and and 1134 English. d gene sequences encoding them, useful treating disorders such as cancer, immune system disorders. φ SEQ ВP Ħ NO:19 5150 217 the

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Sequence 1134 BP;

248 A; 294 C;

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225 T; 0 U; 1 Other;

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04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
10-APR-2002;
10-APR-2002;
11-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                       toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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2002US-0363534P.
2002US-0370248P.
2002US-0371134P.
2002US-0371139P.
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Alignment Scores:
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19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MIL-2002;
09-JUL-2002;
09-JUL-2002;
09-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
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Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 44; SEQ ID NO 430; 874pp; English.
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                                                                                                                                            ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
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                         CCAGTGGAGTGGACAGTCATGGATGTGGTGGTT
                                                                                                                   CCTGGGGCTGATGGGACACCATTTGGCTGTCCTCCTGGGCG
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2002US-0373602P.
2002US-0374139P.
2002US-0378370P.
2002US-0378652P.
2002US-0378655P.
2002US-0378665P.
2002US-0394230P.
2002US-0394230P.
2002US-0407688P.
2003US-0442900P.
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                                                                                                                                                                                                                                                        US-09-976-740-7 (1-217) x ADA53650 (1-1566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Sugiyama
Yamamoto J, Isono Y
Seki N, Yoshikawa T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
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24-JAN-2002; 2002US-0350435P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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DB; ADA55289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; SEQ ID NO 1218; 205pp; English.
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RES ASSOC BIOTECHNOLOGY.
HisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal---
                                                                                                                 ArgGlyPro-----GlnSerAlaLysGluArgValLysGluTrpThrProCysGlyPro
                                                                                                                                                                                                         ValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeu----AsnGlyGlu
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ikawa T,
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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The present sequence is that of a colon specific gene (CSG), designated LSGold gene 407124. This is 1 of 22 claimed CSGs (see ABA91302-23) identified in the Incyte LIFESEQ Gold database using the data mining Cancer Leads Automatic Search Package (CLASP), which identifies highly expressed organ and cancer specific genes. The CSG, or its encoded protein, can be used as a diagnostic marker of colon cancer. The invention provides claimed methods of diagnosing colon cancer, diagnosis metastasis of colon cancer, staging colon cancer, monitoring colon cancer for the onset of metastasis, and monitoring a change in stage of colon monitoring, Colon Macina diagnosis; Colon 08-APR-2002 26-MAY-2000; 29-MAY-2001; 2001WO-US017583 06-DEC-2001 WO200192528-A2 Homo ABA91317; ABA91317 (DIAD-) sapiens 484 194 424 174 364 154 307 134 114 specific polypeptides and polynucleotides useful oring, staging and treating colon cancer. 208 1; Page 110-111; 116pp; English specific colon 94 84 Ŗ DIADEXUS LysProSerAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAla standard; LeuMetGlnArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLys GGATTTGAGGAGCAAGCTAGTGCTTTTCAGGAAACAGGAAATTGATGGAAAATCCCCTGCTA 91 GGCTCTGTCGGTGTAAAAAATTCCATGGAAAAT----ATCTACGAATATCATGTAAAACCTCTGCAGACAAAGCATTTAAAGAACAAC IleTyrGluHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAsp TTGATGACAAGAAATGATGTGTTGACAGGACTTCAGTTAAAATTGGGGGCCTGCTCTGAAA LysProAlaLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGlu GAAGTAAAGGAACCCTGCAGCCTTCCCATGCTATCTGTTGACATGGAAAACAAGGAAAAT -----CCGAGCTCCGCGCGCGCAAACCTCCCGGCGCCCATGCGGGAGTTGCT gene .yPheProGluGlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeu yThrAlaSerValAlaThrGlyProAspSerProSerProValProLeuProProGly - CCACCTGATCCTGCAGACTGGGCCGTGATGGATGTCGTCAATTATTTCCGAACCGTG Chen S, specific 2000US-0207383P (first gene; CSG; gene; human; colon cancer;
therapy; imaging; staging; vaccine; d INC DNA; 1957 entry) gene Pluta 407124. 4 ВР Sun -----PheSerMetAlaAlaMetAsnLysGluGly Ķ Recipon Ξ ds. for diagnosing metastasis, 534 210 ----diagnosing 133 423 153 483 193 173 363 306 300 113 93 207 RESULT 15 AAS75500/ ID AAS7 XX AC AAS7 XX AC AAS7 片 Ş 맑 Ś 밁 Ś 밁 Ś 밁 S 밁 á 밁 8 밁 Ş 밁 Ş 밁 Ş 밁 Ş Best Local S Query Match: SSSSSSSSXX Score: Percent Similarity: 5500/c AAS75500 13-FEB-2002 Sequence 1957 AAS75500 No.: Scores: 832 772 143 683 626 583 349 892 203 183 163 712 123 104 523 467 409 Similarity: 89 76 60 25 standard;

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cancer in a patient, by determining the level of a CSG in a sample of cells, tissues or body fluid and comparing it with the level in a corresponding sample from a healthy human control or from a sample to previously from the patient. Also claimed are methods of identifying therapeutic agents for use in imaging and treating colon cancer. Treatment may involve administering and creating colon dencer appression or activity of a CSG. Adoptive immunotherapy and gene therapeutics may be used. A claimed vaccine for treating colon cancer may be used. es a claimed a sample taken therapy

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> BP; 510 A; 449 ņ 457 <u>ი</u> 541 7, 0 U; 0 Other;

US-09-976-740-7 (1-217) x ABA91317 41 HisGlnLeuAsnGlyGluArgGlyPro-GlnSerAlaLysGluArgValLysGluTrpTh nGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGl GATGGATGTCGTCAATTATTTCCGAACCGTGGGATTTGAGGAGCAAGCTAGTGCTTTTCA GAGACGCCATTCCCGGCTCGGTGAAAAAGGCACTATATCCATC tAsnLys--GluGlySerGluValProGluSer-----AspArgProAla------GlyAlaGlnHis GACAAAGCATTTAAAGAACAAC nGlnGlyHisPheGluAspAsp YLeuSerTleArgLeuGlyProAlaLeuLysTleTyrGluHisHisTleLysValLeuGl GGAACAGGAAATTGATGGAAAATCCCTGCTATTGATGACAAGAAATGATGTTGTGACAGG lmetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGl rProPheGlyCysProProGlyArgLysGluLysProSerAspProValGluFrpThrVa -CCTGCATCGTCTCCAAGACTCATTCCCTCTAAACCTTCAAGTTCCATGGAAAATGGG-rProSerProValPro---LeuProProGlyLysProAlaLeuProGlyAlaAspGlyTh GGCAGCCTGGCGTCTTCTGCCCCTACCGTCCCCTTCTCAGGCCAGTTCTCACTTGCCCCCT rProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAla ACTAAACGCCAGCGAACTGCCTCTCCGTGAAAGTCTTAGCCAGAAACTTTCCCCGCTT--GAGAACGCCACACCTCCACCTTCCACTTTCCAAAGACCGGCTTCCCCGGGGAGCCCCCCAC - TGTCGCCAGTGCCACAGAGAGTCGTGTGGCTCTGGGCCGGCGCTGCTGGTCCAAGA 5.61e-09 300.00 50.48% 38.94% 25.64% -----ProGlySerGlyThrArgGlnValPheSerMetAlaAlaMe (1-1957) -GluGlyGlyThrAlaSerValAlaThrGlyProAspSe 913 210 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: -----AGACCÁCCTGATCCTGCAGACTGGGCCGT 1957 81 24 62 81 104 522 831 183 771 163 143 682 123 625 582 89 466 60 408 40 711 75

cDNA; 483

ВP

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

DNA encoding novel human diagnostic protein #11304

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) CC sequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a golypeptide in tissue, as molecular weight markers and as a food consisted the sequences of the involving aberrant protein expression or biological activity. The conversation of the sequences have applications in diagnostics, forensics, gene mapping, identification of mutations creations of the produce other types of data and products dependent on DNA and continuously sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in continuously from Wipo at continuously that and incoming format directly from Wipo at continuously the continuously of the sequence of the involving aberrant protein wipo at the printed specification, but was obtained in the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 11304; 103pp; English.
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336 GAAAAT--
                                 103 AspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGly 122
                                                                      396
                                                                                        83 ValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyPro ::: |||::: |||
                                                                      ATGCTATCTGTTGACATGGAAAACAAGGAAAATGGCTCTGTCGGTGTAAAAAATTCCATG 337
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                                                                                                                                                                               0 Other;
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	120 CAGACAAAGCATTTAAAGAACAAC 97	밁
	203 GlnGlnGlyHisPheGluAspAsp 210	Ş
raaaaccrcrc 121	80 GGACTTCAGTTAAAATTGGGGCCTGCTCTGAAAATCTACGAATATCATG	밁
leLysValLeu 202	183 GlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeu 202	Ş
ATGTGTTGACA 181	40 CAGGAACAGGAAATTGATGGAAAAATCCCTGCTATTGATGACAAGAAATG	벍
3pValLeuThr 182	163 GlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThr 182	δ
TAGTGCTTTT 241	00 GTGATGGATGTCGTCAATTATTTCCGAACCGTGGGATTTGAGGAGCAAG	멍
laThrAlaPhe 162	143 ValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPhe 162	Ś
CAGACTGGGCC 301	330GGGAGACCACCTGATCCTGCAGACTGGGCC 301	멍
alGluTrpThr 142	123 ThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThr 142	Ş

Search completed: March 12, 2004, 21:08:21 Job time: 357.96 secs

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Command line parameters:

MODEL-Eframe+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPT0_spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-Q=/cgn2_1/USPT0_spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
-DB=GenEmbl -OpWT=fastap -SUFFIX=rye -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UTPMT=pto -NORM=ext -HBAPSIZE=500 -MINLENN=0 -MAXLENN=200000000
-USER=US09976740_@CGN 1_1 9705 @runat 10032004_094548_19540 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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       Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_cther:*
32: em_htg_cther:*
33: em_htg_mus:*
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41: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

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                                                                                                  gene
                          CDS
                                                                                                                                                                                                                                                                                                                             source
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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WcKlernan, K.J., Malek, J.A., Gourath, J., Green, E.D.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

12280, 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
IMAGE:3677194), partial cds.
                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 24 Row: g Column: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 20, 2003 this sequence version replaced gi:13938477
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                                             /db_xref="LocusID:90378"
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\lambda_xref="taxon:9606"
\lambda_nne="IMAGE:3677194"
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ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly
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US-09-976-740-7 (1-217) x BC007384 (1-982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GAAGAGCGAGTACTTGAGAAAGAAGAAGAAGATGATGATGAAGATGAAGATGAAGAT
                                       LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLySIleTyrGluHisHisIleLys
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                                                                                                                                       AlaPheGlnGlnGlnGlpIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal
                                                                                                                                                                                                                                            TrpThrValMetAspValValGluTvrPheThrGluAlaGlyPheProGluGlnAlaThr
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                                                                                                                                                                                                       TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA
                                                                                                                                                                                                                                                                                                                GACGGGACCCCCTTTGGCTGT
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TYMDVVEYFTEAGFPEGATAFQEQEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHHI
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona,
Lees, A.M. popprotein binding proteins a

Low density lipoprotein binding proteins a

diagnosing and treating atherosclerosis

Patent: US 6355451-A 16 12-MAR-2002;
            TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr
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                                                 AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal
                                                                                   TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCCGGAGCAGGCGACA
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/mol_type="genomic DNA"
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Low density liprotein binding proteins
and treating atherosclerosis
Patent: WO 01648974-A 16 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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/proteIn_id="CAC88296.1"
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Eukaryota; Metazoa; Cnidaria;
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                            GGGCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC
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/mol_type="genomic DNA"
/db_xref="taxon:6100"
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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
RS Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Laric,P., Legaspi,R.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloekey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: m Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
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Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replac
Contact: MGC help desk
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                                                        /gene="IOC90378"
/note="SAM; Region: Sterile alpha motif. Widespread domain /note="SAM; Region: Sterile alpha motif. Widespread domain in signalling and nuclear proteins. In EPH-related tyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"
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rtranslation="gaarpvsllevvrylggsggaggrltrgrvogilebebebeddvs
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wtvmdvveyfteagfpegatafqeegeidgkslllmqrtdvltglsirlgpalkiyeh
                                                                                                                                                                                                                                                                                                                             IKVLQQGHFEDDDPDGFLG"
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/db_xref="GI:33871479"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="LOC90378"
/db_xref="LocusID:90378"
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_xref="taxon:9606"
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Lees, A.M., Lees, R.S., Law, S.W. and Arjon:
Low density lipoprotein binding proteins
diagnosing and treating atherosclerosis
Patent: US 6632923-A 45 14-OCT-2003;
                                                                                                                                                                                               Sequence 45
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                                                                                       Law, S.W. and Arjona, A.A.
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s,A.M., Lees,R.S., Law,S.W. and Arjona,A. density liprotein binding proteins and treating atherosclerosis ent: WO 0164874-A 45 07-SEP-2001;
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용	964 GAAGAGCGAGTACTTGAGAAAGAAGAGGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAAGAT
¥.	21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
용	1024 GATGATGTCAGAGGGCCTCTGAAGTGCCCCGAGAGTGACCGTCCTGCAGGGTGCCCAGCAC 1083
γ	41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
용	1084 CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGGGTCAAGGAGTGGACC 1143
Ŋ	61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80
용	1144 CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGCCAGCCCCGGGCAGCCAGC
Ŋ	81 ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
용	1204 CGCCAGGTGTTCTCCATGGCAGCATGAACAAGGAAGGGGGAACAGCTTCTGTTTGCCACC 1263
γ	101 GlyProAspSerProSerProValProLeuProGryLysProAlaLeuProGlyAla 120
용	1264 GGGCCAGACTCCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC 1323
γ	121 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
8	1324 GACGGGACCCCCTTTGGCTGTCCGCCCGGGCGCAAAGAGAAAGCCATCTGATCCCGTCGAG 1383
¥	141 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
B	1384 TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGCAGCAAA 1443
Ϋ́	161 AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuCtGlnArgThrAspVal 180
g	1444 GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG 1503
Υς	181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 200
ğ	1504 CTCACCGGCCTGTCCATCCGGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG 1563

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Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
Atherin, a newly identified LDL-binding protein in human atherosclerotic lesions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deconinck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
Direct Submission
Submitted (30-OCT-2003) Harvard-MIT Division of Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa;
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  HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr
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LGPALKIYEHHIKVLQQGHFEDDDPDGFLG"
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/chromosome="19"
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1362)
Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 6355451_A 12 12-MAR-2002;
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Sequence 12 from patent US 6355451
AR199531 GI:20249605
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1 (bases 1 to 1362)
Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and tidiagnosing and treating atherosclerosis
Patent: US 6605588-A 12 12-AUG-2003;
Location/Qualifiers
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6632933-A 12 14-CCT-2003;
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1. .1362
                                                                                                                                         /organism="unknown"
/mol_type="genomic
                                                     7.08e-48
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Oryctolagus cuniculus (rabbit)
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Oryctolagus cuniculus
Bukaryota, Metazoa, Chordata, Craniata, Ver
Mammalia, Eutheria, Lagomorpha, Leporidae,
                                                                                                                                                                                                                                                                                                       Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density liprotein binding proteins and the
and treating atherosclerosis
Patent: WO 0164874-A 12 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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         /organism="Oryctolagus
/mol_type="unassigned D
/db_xref="taxon:9986"
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Aequorea Aequorea: Eukaryota; Metazoa; Chidaria; nyununa
Aequoreidae; Aequorea.
1 (bases 1 to 1362)
1 (bases 1 to 1362)
Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Novel low density lipoprotein binding proteins
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                                                                                                                                               Aequorea victoria
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AX239569 Sequence 12 AX239569 AX239569.1

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VERSION KEYWORDS

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REFERENCE AUTHORS TITLE

FEATURES

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BOSTON HEART FOUNDATION INC
PN JP 2001506983-A/3
PD 29-MAY-2001
PF 26-NOV-1997 JP 1998524870
PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC
A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC
C07H21/00,
PC C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC
Strandedness: Single;
CC Topology: Linear;
FH Key , LOCation/Qualifiers.
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                                                             ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis
                                                                                            CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC
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                                               ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCAGCGTTGAAAATCTATGAGCAC
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1. .1362
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/mol_type="genomic DNA"
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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model p/US09976740/runat 10032004 094549 19564/app query.fasta_1.1898
-Q=/cgn2 1/USPTO_spool_p/US09976740/runat 10032004 094549 19564/app_query.fasta_1.1898
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -TRR SCORE=pct -TRR MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -CUTRMT=pco -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=200000000
-USER=US09976740 @CGN 1 1 235 @runat 10032004 094549 19564 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG-SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOD=6
-FGAPEXT=7 -YGAPOD=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                             RESULT 1
US-08-979-608A-16
; Sequence 16, Applicatio...
; Patent No. 635451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
Arjona, Anibal A.
Arjona, Anibal A.
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US-09-620-312D-638
US-08-974-380-1
US-08-954-466-1
US-08-952-153-7
US-08-852-153-7
US-08-852-153-3
US-08-852-153-3
US-08-852-153-3
US-08-852-153-3
US-08-852-153-3
US-08-852-153-3
US-08-852-153-3
US-09-616-289-31
US-09-617-849-31
US-09-617-849-31
US-09-894-998A-35
US-09-118-29A-6
US-09-118-930-218
US-09-118-930-218
US-09-118-930-218
US-09-118-930-218
US-09-115-537-3
US-09-115-537-3
US-09-114-908-1
US-09-141-908-1
US-09-155-87-5
US-09-141-908-1
US-09-657-440-19
S215881-2
US-07-945-283-1
Sequence 11, Appl Sequence 50, Appl Sequence 50, Appl Sequence 638, Appl Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 31, Appli Sequence 31, Appli Sequence 8, Appli Sequence 8, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 218, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 10, Appli Sequence 11, Appli Sequence 5, Appli Sequence 5, Appli Sequence 19, Appli Sequence 19,
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STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
PILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
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LOCATION: 1...651

SEQUENCE DESCRIPTION: SEO TO FOR US-08-979-608A-16
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              RESULT 2
US-09-517-849-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPAX: 617/542-8906
                                                          601
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                                                                                                                                                                                                                                                                                                                                                          GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                        GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC
                                                                             ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly
                                                                                                                                                                                          AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal
                                                                                                                                                                                                                                              TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr
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                                                                                                                 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG
                                                                                                                                 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys
                                                                                                                                                                       GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG
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 Application
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Matches:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 1079
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8076
TELEPAX: 617/542-8066
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTMARE: FABLESEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID
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                                                                                HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
                                                                                                                            GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCAGCAC
                                                                                                                                                                                                                  GluGluArgValLeuGluLysGluGluGluGluAspAspAspAspGluAspGluAspGluGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr
                                                             CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC
                                                                                                                                                     AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40
                                                                                                                                                                                               LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
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OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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Law, Simon W.
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Matches:
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Mismatches:
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SOFTWARE: FastSEQ for Wi
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-09-616-289-16
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 60/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-616-289-16
; Sequence 16, Applica;
; Patent No. 6632923
; GENERAL INFORMATION:
                                                                                                             Percent Similarity:
Best Local Similarity:
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    GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluAspGluGlu
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US-09-616-289-45
; Sequence 45, Appl
; Patent No. 663292
                                                                                                                             APPLICANT: ALJONA, ANIBAL A.

APPLICANT: ALJONA, ANIBAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1900-03-02

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION DATE: 1997-06-03
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NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Wir
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Percent Similarity:
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                                                                                                                                                              Sequence 12, Application Patent No. 6355451 GENERAL INFORMATION:
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Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR US!
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 07-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Seq
LOCATION: 1...696
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                      118
                                                                                                                     277
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                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 Franklin Street
CITY: Boston
STATE: MA
 ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp 137
                                                                               ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAiaLeu 117
                                                                                                                                         SerGlyThrArgGlnYalPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
                                                                                                                                                                                                                                                                         GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluArgValLys
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                   CAGTGGTCGCTGTGGCCCCCACCCTGGCCAGGAGGAAGGGCCGGGGGCCGGCGGGC
                                                                                                                                                                                                           GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly
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1047.50
95.45%
88.64%
89.53%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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195
15
3
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77

276

57 156 38 96 20

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RESULT 6
US-09-517-849-12
; Sequence 12, Application US/09517849
; Patent NO. 6605588
; GENERAL INFORMATION:
    APPLICANT: Lees, Ann M.
    Lees, -Robert S.
                                                                                                                NAME/KEY: Coding Sequence;
LOCATION: 1...696;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-517-849-12
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        Percent Similarity:
Best Local Similarity:
                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                           COMPUTER: IMPORTED COMPUTER: IN COMPARISH COMPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Max-2000
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 12:
GRADITENCE COMPARITON SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING

TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuLeuMetGlnArg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAG 516
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                                                                                                                                                                                                                                TOPOLOGY: linear
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      1.45e-76
1047.50
95.45%
88.64%
      Length:
Matches:
Conservative:
Mismatches:
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US-09-616-289-12
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PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILLING DATE: 2000-03-02
PRIOR PELLOATION NUMBER: US 08/979,608
PRIOR FILLING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PELLOATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILLING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Patent No. 60
                                                                                                                                                                                 APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
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; NAME/KEY: CDS
; LOCATION: (1)...(696)
US-09-616-289-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1362
TYPE: DNA
ORGANISM: Oryctolagus
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ENGTH: 1362
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: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
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1047.50
95.45%
88.64%
89.53%
                                                                         US/08979608A
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COURTENT LAPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 60/979,608A

FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: US 60/031,930

FILING DATE: 35-965

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (£0.2001)

TELEPHONE: 617/542-8906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
337
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                                                                                                                                   GlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLySGluArgValLys
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SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
                                                                  GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly
                                                                                                                                                                                                     GACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCG
                                                                                                                                                                                                                       AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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1047.50
95.45%
88.64%
89.53%
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE

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US-09-517-849-13
(US-09-517-849-13); Sequence 13, Application
; Patent No. 6605588
; GENERAL INFORMATION:
                                             COMPUTER REAL/ADDICATE DISKETTE

MEDIUM TYPE: Diskette

COMPUTER: 1EM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION UNDRER: US/09/517,849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION UNDRER: 08/979,608

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: MYSTE, LOLIS

REGISTRATION UNDRER: 35,965

REFERENCE/DOCKET NUMBER: 10797-003001

TELEOMOMUNICATION INFORMATION:

TELEPHONE: 617/542-8906

INFORMATION OFOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 1422 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
     NAME/KEY: Coding Sequence LOCATION: 1...756
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPECT FISH & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
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Law, Simon W.
Arjona, Anibal A.

ANIONE NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USI TREATING ATHEROSCLEROSIS
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Sequence 13, Application US/09616289

Patent No. 6632923

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Annon M.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: ANJOHA AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979 608
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Pred. No.:
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Matches:
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Best Local Similarity:
Query Match:
DB:
RESULT 11
US-08-979-608A-11
; Sequence 11, Ap
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; NAME/KEY: CDS
; LOCATION: (1)...(756)
US-09-616-289-13
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PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1422
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                              CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCG
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    Application US/08979608A
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Matches:
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: ISM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/979,608A
FILING DATE: 26-No. 635451-1997
PRIOR APPLICATION UNMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 03-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 10797-002001 (fc
REFERENCE/DOCKET NUMBER: 10797-002001 (fc
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
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GENERAL INFORMATION:
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No.:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ
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MEDIUM TYPE: Diskette
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                                                                                                   CAGCATCACCAGCTGAATGGCGGCGAGCGCGGCAGACCGCCAAGGAGCGGGCCAAG 471
                                                                                                                         GACGACGACGTCTCTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCG
                                                                                                                                                                                              AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
{\tt SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer}
                                  GAGTGGTCGCTGTGTGGCCCCCCCCCCCCCGCCCAGGAGGAGGAAGGGCCGGGGGCCGGCCGCGGGC
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OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                              1.81e-76
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RESULT 12
US-09-517-849-11
; Sequence 11, Application
; Patent No. 6605588
; PATENT INFORMATION:
; APPLICANT: Lees,
       STREET: 22...
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASKSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/517,849
FILING DATA:
APPLICATION NUMBER: 08/979,608
FILING DATA: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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   US-09-517-849-11
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
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Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lees,
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Ary Simon W.
APPLICANT: Aryona, Anibal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FULE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
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Patent No. 6632923
                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 GlnHisHisGlnLeuAsn----GlyGluArgGlyProGlnSerAlaLysGluArgValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla
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Matches:
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; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)...
US-09-616-289-11
RESULT 14
US-09-616-289-48
; Sequence 48, A)
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TYPE: DNA
ORGANISM: Oryctolagus
FEATURE:
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                                                                                                                                                ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCAGCGTTGAAAATCTATGAGCAC
                                                                                                                                                                                                                      CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC
                                                                                               leLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Ariona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 2561
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEARURE:
NAME/KEY: CDS
LOCATION: (246)...(1895)
US-09-616-289-48
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                                                                                                 CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAAGCCGGCAGAC
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Matches:
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80 4456	Qy 61 ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr	U . D
60 4396	Qy 41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr	u o
40 4336	Qy 21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis	U D
20 4276	Qy 1 GluGluArgValLeuGluLysGluGluGluGluAspAspGluAspGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluG	a vo
	US-09-976-740-7 (1-217) x US-09-616-289-50 (1-12425)	Ϥ
	Alignment Scores:  1.87e-74  Pred. No.:  1.036.50  Matches:  216  Percent Similarity:  Best Local Similarity:  4.88.598  DB:  1.87e-74  Maches:  216  Conservative:  0  Mismatches:  1  Gaps:  3	<b>ל</b> רמר <b>ש</b> סט
	; SEQ ID NO 50 ; LENGTH: 12425 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-616-289-50	g
	PRIOR FILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 53 SOFTWARE: FASTSEQ for Windows Version	
	FRIOR FILING DALE: 1397-11-20  FRIOR APPLICATION NUMBER: US 60/031,930  FRIOR FILING DATE: 1996-11-27  FRIOR APPLICATION NUMBER: US 60/048,547	
	PRIOR FILING DATE: 2000-03-02  PRIOR APPLICATION NUMBER: US 08/979,608  DETOR ETLING DATE: 1007-11-26	
	CURRENT APPLICATION NUMBER: US/09/61 CURRENT FILING DATE: 2000-07-14 DETOR ABBLICATION NUMBER. US 00/617	
	APPLICANT: Law, Simon W. APPLICANT: Law, Simon W. APPLICANT: Arjona, Anibal A. TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: APPLEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS	
	RESULT 15 US-09-616-289-50 US-09-616-289-50 , Sequence 50, Application US/09616289 , Patent No. 6632923 , GENERAL INFORMATION: , APPLICANT: Lees, Ann. M.	
 1895	Db 1836 CATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA	U
 217	Oy 198 HisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly	O
 197 1835	Oy 178 ThraspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis	a o
177 1775	Oy 158 GlnAlaThrAlaPheGlnGluGlnGluIleAepGlyLysSerLeuLeuLeuMetGlnArg	D 10

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isPheGluAspAspAspProAspGlyPheLeuGly 217	leArgieuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGlyH 206 	lulleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerI 186	cagagggccTcccTgggaTgTgccCTgaTcccGgcTTTCTCTGTTCCTGTCCCACCCAGG 4995	InalaThralaPheGlnGlu 164 	roValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluG 158 	TGTTCACTGGTGTCTGTTTGTTTTGATGCAGTCCCGGGGGCAAAGAAGAAGCCATCTGATC 4816	TGGGGTATTGGAGACATGGGGGTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCG 4756	UPTOPTOGIYLYSPTOAlaLeuPTOGIYAlaAspGlyThrPTOPheGlyCysPTO 128	GTTTTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCCGTCCCCCGTGCCTTT 4636	GGGTGGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCGAAGACAAAGCCAAAGACAGGT 4576

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-DB=PublIshed_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62

-TRANS-human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MX=100

-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXIEN=2000000000 -USER=US09976740 @CGN 1 1712 @runat 10032004 094549 19588

-NCPU=6 -ICPU=3 -NO_MNAP -LARGBOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -

-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-5ep-2001
PRIOR APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-5ep-2001
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/ACENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (forme)
TELECOMMUNICATION INFORMATION:
TELEPRAY: 617/542-5070
TELEPRAY: 617/542-5070
TELEPRAY: 617/542-50906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180
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; Publication No.
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APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

ITITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/034,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR TILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-976-740-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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LENGTH: 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo s
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...
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                                ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr
                                                                                          ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr
                                                                                                                                                  CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGGTCAAGGAGTGGACC
                                                                                                                                                                       HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 60
                                                                                                                                                                                                                             GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC
                                                                                                                                                                                                                                                                                                   CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC
                                                                            CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGCAGCGGCACC
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APPLICANY: LAW, SIMOL T.
APPLICANT: APPLICANT: ANJOHA A.
APPLICANT: AFONA, ANIDAI A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY
TITLE OF INVENTION: ATHERSECLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/034,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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                                                              US-09-976-740-7 (1-217)
                                                                                               Query Match:
DB:
                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               Alignment Scores: Pred. No.:
                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-671-242-16
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US-10-671-242-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
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US-10-023-529-16
; Sequence 16, App
; Publication No.
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                                                            SOFTWARE: FastSEQ
SEQ ID NO 16
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                             ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly
                                                                                                                               LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys
                                                                                                 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG
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US-10-023-529-16

(Sequence 16, Application US/10023529

Publication No. US20020129388A1

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: LAW, Simon W.
APPLICANT: LAW, Simon W.
APPLICANT: NATION AND THEIR USE IN DIAGNOSING AND THILE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001

CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/10/023,529

CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/046,547
PRIOR APPLICATION NUMBER: US 60/046,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

AND TREATING

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Sequence 16, Application US/10023523

| Publication No. US20020152485A1
| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M.
| APPLICANT: Lees, Robert S.
| APPLICANT: Lees, Robert S.
| APPLICANT: Law, Simon W.
| APPLICANT: Law, Simon W.
| APPLICANT: Arjona, Anibal A.
| ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING:
| TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS
| TITLE OF INVENTION: ATHEROSCLEROSIS
| CURRENT APPLICATION NUMBER: US/10/023,523
| CURRENT FILING DATE: 2001-12-17
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (1)...(651)
US-10-023-529-16
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US-10-023-523-16
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PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER: OF SEQ ID NOS: 53
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-616-187-16
US-10-616-187-16
; Sequence 16, Application US/10616187
; Publication No. US20040013668A1
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PRIOR FILING DATE: 2000-03-02
PRIOR PPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
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APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
TILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
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Publication No. US2003005588A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20030055588A1el Nucleic Acid Molecules Encoding
TITLE OF INVENTION: Nucleic Acid and Protein Homologs
FILE REFERENCE: 35800/237985
CURRENT FILING DATE: 2001-08-29
UNMBER OF SEQ ID NOS: 65
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SEQ ID NO 6
LENGTH: 1445
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                                                                                                                       ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr
AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ITITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ITITLE OF INVENTION: ATHEROSCLEROSIS
ITITLE OF INVENTION UMMERS: US/09/976,740
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 1000-07-14
PRIOR FILING DATE: 1000-07-14
PRIOR APPLICATION NUMBER: US 60/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1096-11-27
PRIOR FILING DATE: 1096-11-27
PRIOR FILING DATE: 1097-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-976-740-45
                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-976-740-45
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                                                   GATGATGTGAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 1083
                                                                             AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis
                                                                                                                  GIGCITCAGCAAGGCCACTITGAGGATGATGACCCCGATGGCTTCTTAGGC 836
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                                                                 ; ORGANISM: Homo sa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ...(
US-10-671-242-45
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US-10-671-242-45
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Publication No.
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: PROTEINS AND THE USE IN DIAGNOSING AND
TITLE OF INVENTION: PROTEINS AND THE USE IN DIAGNOSING AND
TORRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/034,547
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTMARE: FastSEQ for Windows Version 4.0
SOFTMARE: FastSEQ for Windows Version 4.0
TYPE: DNA
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RESULT 10

US-10-023-529-45

US-10-023-529-45

Sequence 45, Application US/10023529

Publication No. US20020129388A1

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Ann M.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: AIJona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THER USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT APPLICATION NUMBER: US/616,289

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930
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Best Local Similarity:
Query Match:
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   RESULT 11
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; Publication No. US20020152485A1
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; NAME/KEY: CDS
; LOCATION: (1)...
US-10-023-529-45
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PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 45
LENGTH: 1614
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ORGANISM: Homo
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ANTHROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,523

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 09/99,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-06-03

NUMBER: OS 580,000 SEQ ID NO 45

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US-10-023-523-45
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SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-10-616-187-45
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APPLICANT: Lew, SIMON W.
APPLICANT: Law, SIMON W.
APPLICANT: Ariona, Anibal A.
APPLICANT: Ariona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ARTHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/616,187
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1907-11-26
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
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US-10-616-187-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober APPLICANT: Law, Simon APPLICANT: Arjona, Ani
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                                                     CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 1142
                                                                                                                                GATGATGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC 1083
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TITLE OF INVESTIGE 0.1.

FILE REFERENCE: PA103P1C1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION PATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: PATE: 1326
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Query Match:
DB:
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US-10-102-806-247
US-10-102-806-247, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
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LOCATION: (1336)
OTHER INFORMATION: n equals a,t,
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LOCATION: (26)_
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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                          GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluAspGluGlu
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US-09-962-055-12
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COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: PastSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CORRESSPONDENCE ADDRESS:
CORDESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                    Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 27-NOV-1996
ATTORNBY/AGENT IMPORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
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                                                                     ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis
                                                                                                         CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGCAAGTCCCTGCTGCTCATGCAGCGC
                                                                                                                         GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuLeuMetGlnArg 177
                                                                                                                                                                              ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157
                                                                                                                                                                                                                                     ProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp 137
                                                                                                                                                                                                                                                                                       ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
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                                                                                                                                                                                                                                                                                                                                                                                  CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAAGCCGGCAGAC
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S-Guence 12, Appilute 133A1; Sequence 12, Appilute 134633A1; Publication No. US20020194633A1; GENERAL INFORMATION: Lees, Ann M. APPLICANT: Lees, Robert S. APPLICANT: Law, Simon W. Appilute 14 Applicant 14 Applicant 15 Applicant 16 Applican
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APPLICANT: ATJONA, ATIOAL A.

APPLICANT: ATJONA, ATIOAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: ATHEROSCISCISCOSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR PRILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILLING DATE: 1997-06-03
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US-09-976-740-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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US-09-976-740-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1362
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CCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAGAAGCCGGCAGAC
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                                                                                                                                ValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
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	Search completed: March 13, 2004, 04:26:11 Job time : 319.946 secs	Sear Job
96	637 CATATCAAGGTGCTGCAGGAGGTCACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 6	망
17	198 HisIleLysValLeuGlnGlnGlyHispheGluAspAspAspProAspGlyPheLeuGly 217	\$
36	577 ACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGGCCAGCGTTGAAAATCTATGAGCAC 6	Ъ
97	178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197	Ş
76	517 CAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGCAAGTCCCTGCTGCTCATGCAGCGC 5	Ф
77	158 GlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg 177	\$
16	457 CCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGCTTCCCTGAG 516	В
57	138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 157	8

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_/USPF7_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-Q=/cgn2_P/IUSPF7_spool_p/US09976740/runat_10032004_094548_19551/app_query.fasta_1.1898
-DB=EST -QFMT=fastap -SUFF1X=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTENT=pto -NORM=ext -HEAPSCISE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09976740 @CGN 1 1 10232 @runat 10033004 094548 19551 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
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Ygapop 10.0 , )
Fgapop 6.0 , I
Delop 6.0 , I
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	9	38	37	96	<b>3</b> 5	ω 4	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	<u>,</u>	٠,	1. E		10	9	00	7	თ	ហ	4.		N	<b>1</b>	Result No.	
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## ALIGNMENTS

REFERENCE	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BE270805 LOCUS DEFINITION
minaryota; metazoa; chordata; cianiata; vertebrata; Eutereostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1109)	Homo sapiens (human) Homo sapiens	mENA sequence. BE270805 BE270805.1 GI:9144449	BE270805 1109 bp mRNA linear EST 13-JUL-2000 600943804F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966449 5',

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM69 row: h column: 02
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                           TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
                                                                                                                                                 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 140
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/lab_host=="DH108 (phage-resistant)"
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21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM352 row: f column: 11
High quality sequence stop: 709.
Location/Qualifiers
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Tissue Procurement: Louis M. Staudt,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                             GluGluArgValLeuGluLysGluGluGluGluAspAspAspAspGluAspGluAspGluGlu 20
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                                      CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG
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adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8bb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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1095.50
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98.60%
93.63%
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Primates;
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                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (Dases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                              e: LLCM1866 row: h column: 15 quality sequence stop: 785.
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5095742"
/tissue_type="Burkitt lymphoma"
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    996 bp
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5', mRNA sequence.
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BU174966.1 GI:22688950
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COMMENT

SOURCE

FEATURES

mRNA linear EST 04-SEP-2002 sapiens cDNA clone IMAGE:6087267

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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 8"
/clone = "Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Length:
Matches:
Conservative:
Mismatches:

US-09-976-740-7 (1-217) x BI226646 (1-785) 119 GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluAspGluGlu ValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLySIleTyrGluHisHisIleLys TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr GGGCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC GTGCTTCAGCAAGGCCACTT-GAGGATGATGACCCCGATGGCTTCTTAGGC CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCA-CACATCAAG GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal TGGACCGTGATGGATGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACA GÁCGGGAC-CCCTTTGGCTGTCCTCCCGGGCGCAAAGAGAAAGCCATCTGATCCCGTCGAG CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGGCAGCCCGGGCAGCGGCACC Indels: Gaps: 785 214 0 217 706 160 140 120 100 118 40 200 180 537 477 418 358 298 80 238 60 178 597 20

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2323 row: j column: 04
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Eukaryota;
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                                              GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120
                                                                                                                                             ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 100
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Location/Qualifiers
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/lab host="DHIOB (phage resistant)"
/clone lib="NHI MCC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI, cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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db_xref="taxon:9606"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12059 row: k column: 05
High quality sequence stop: 752.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
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Tissue Procurement: DCTD/DTP
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603638922F1 NIH_MGC_87 Homo sapiens
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(1-217)
                                                                                                                                                                                                                                                                                           /tissue_type="mammary adenocarcinoma, cell line" /lab host="DH10B (phage-resistant)" /clone_lib="NIH MGC_87" /clone_lib="NIH MGC_87" /clone_lib="NIH MGC_87" /clone_Topan: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oilgo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5415292"
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                                                         Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2379 row: o column: 17

High quality sequence stop: 538.

Location/Qualifiers
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AGENCOURT 8032664 NIH MGC 102
5', mRNA sequence
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BQ671165
                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6213736"
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601315608F1 NIH_MGC_8 Homo
mRNA sequence.
BE513784
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US-09-976-740-7 (1-217) x BQ671165 (1-921)
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GGGCTTTCCGCAGGCCCCTTTGAGGGGTGATGACCCCGAGGGCTTCTTA
                                                          ValLeuGln-GlnGlyHisPheGlu-AspAspAspProAspGlyPheLeu
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//lab host="DHIOB (phage-resistant)"
//clome_lib="NIH_MGC_102"
//clome_lib="NIH_MGC_102"
//note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
//note="Organ: salivary gland; Vector: pOTB7; Site
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686 bp mRNA no sapiens cDNA

clone

linear EST 07-AUG-2000 ne IMAGE:3634417 5',

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AUTHORS
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratiom
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM328 row: p column: 02
High quality sequence stop: 642.
Location/Qualifiers
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                            yProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAlaAs 121
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/lab_host="NBH108 (phage-resistant)"
/lab_host="NBH108 (phage-resistant)"
/clone_lib="NHH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: RocRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: McC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9688 row: g column: 10
High quality sequence stop: 590.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini;
1 (bases 1 to 590)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.go
Tissue Procurement: ATCC
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BE621115
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/tissue type="epithelioid carcinoma"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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/db_xref="taxon:9606"
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26 GlySerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGly

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K-EST0072322 S22SNU16n1
5', mRNA sequence.
                                                                                            Email: yongsung@mail.kribb.re.kr
Plate: 15 row: C column: 02
High quality sequence stop: 568.
Location/Qualifiers
                                                                                                                                                             Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eceun-dong Yuscong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                          Kim, Y.S.
21C Frontier Korean EST
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1 (bases 1 to 568)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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                                                                                                                                                                                                                                                Contact: Kim YS
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                                                                                                                                                                                                                                                                423 GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC
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602396526F1 NIH
mRNA sequence.
EG298788
EG298788.1 GI:
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                                           1056 bp n
NIH_MGC_94 Mus musculus
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/clone lib="\$22SNU16n1"
/clone lib="\$22SNU16n1"
/note=Torgan: Stomach; Vector: pT773-Pac; Site 1: EcoRI;
Site 2: Not1; The \$22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Sorean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.

ORIGIN	(1990), Cancer Res 50: 2773-2780."	
Alignment Sco	cores: 7 ole-55 Length.	
Score:	Matches:	
Percent Simil	100.00% Conservative:	
Best Local Similarity:	100.00% Mismatches:	
Query Match:	87.35% Indels:	
DB:	12 Gaps:	
US-09-976-740	6-740-7 (1-217) x BM792162 (1-568)	
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Db 3	3 GAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCACCAGCTTAACGGCGAGCGG	ନ-
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Db 63	63 GGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCCTGCGGACCCCCACCAGGGC	g-
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Db 123	123 CAGGATGAAGGGCGGGGCAGCCCGGGCAGCGGCACCCGCCAGGTGTTCTCCATGGCA	Ğ-
Оу 88	88 AlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerPro	-8 -8
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Оу 108	108 ValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGlyCys	S
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Qy 128		_ b_
Db 303	303 CCTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGTCGAGTGGACCGTGATGGATG	ä-
Qy 148		_L _e
Db 363	363 GAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACAGCTTTCCAAGAGCAGGAAATT	13-
Qy 168	168 AspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerIleArg	- <u>i</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10394 row: c column: 08
High quality sequence stop: 752.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko_Laboratory
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technolog cDNA Library Arrayed by: The I.M.A.G.E.
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                                                                                                                                                                                                                      SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer 97
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                                                                                                                                                                                                 AGCTGCACACGGCAGGTGTTCCCCGATGACAGCTGTGAATAAAGAAGGGGGATCAGCTTGT 251
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Eutheria;
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M.A.G.B. Consortium
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 774)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: ATCC/DCTD/DTP
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mRNA sequence
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B1987692 1 GI:
EST
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Nucl
                                                                                                                                               Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                 Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 600)
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                                         /mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5
/clone_lib="Mouse E14.5 retina
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ZECRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
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US-09-976-740-7 (1-217) x BF058975
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Best Local Similarity:
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High quality sequence stop: 495.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Micha
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalla; Eutheria; Primates; Catarrhini; Hom 1 (bases 1 to 704)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                              GATGATGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCAC
                                                                                   AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis
                                                                                                                                           GluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluAspGluGlu
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/db_xref="taxon:9606"
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AUTHORS
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B1985158
B1985158.1 GI:17956088
EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                             Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030,
Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M. (bases 1 to 600)

Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H. Gene expression in the developing mouse retina by EST sequencin
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Nucleic Acids Res. 29 (
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                                                                                                                             /organism="Mus musculus"
/mol type="mRNA"
/db_xref="raxon:10090"
/tissue type="neural retina"
/dev_stage="embryonic day 14.5 pu
/clone_lib="Mouse E14.5 retina li
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                                                                                                                             ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGinGluGln
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                                                     GAAATTGATGGCAAGTCTTTGTTGCTCATGCAACGGACAGATGTGCTCACTGGCCTATCC
                                                                     GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer
                                                                                                           GTGGTGGAATACTTCACTGAGGCGGGCTTCCCAGAGCAGGCCACTGCTTTTCAAGAGCAG
                                                                                                                                                                                                                     TCTCCGGTGCCTTTGCCTCCAGGAAAACCAGCCCTACCTGGGGCTGATGGGACACCTTTT
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ATCCGCCTGGGCCCAGCCCCTGAAGATCTACGAGCACCACATCAAGGTGCTTCAGCAA
              IleArgLeuGlyProAla-LeuLysIleTyrGluHisHisIleLysValLeuGlnGln
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Search completed: March 13, Job time: 3293.03 secs 2004, 04:01:30

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Command line parameters:

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-(MODEL=frame+ p2n.model -DEV=xlp
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-Q=/cgn2 1) (USPTO gpool p/US09976740/runat 10032004 094548 19540/app_query.fasta_1.1898
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-UNITG=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=human40.ddi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-CUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXXEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-DEV TIMEOUT=17 -YGAPOP=10 -YGAPOP=10 -TGAPOP=10 -YGAPOP=10 -TGAPOP=10 -T
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 6605588-A 30 12-AUG-2003;
Location/Qualifiers
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Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6355451-A 30 12-MAR-2002;
Location/Qualifiers
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Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 6632923-A 30 14-OCT-2003;
Location/Qualifiers
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Query Match:
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Requoreidae; Aequorea.

Rovel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis

patent: JP 2001506983-A 10 29-MAY-2001;

BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/10

PF 26-NOV-1997 JP 1998524870

PR 27-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI

ARIX M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC

A61X38/04, A61X38/17, A61X39/00, A61X48/00, A61X49/00, A61X51/08, PC

C07H21/00,

PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Jeffel Contain/Qualifiers.
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Aequorea victoria
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BD056452.1 GI:22602058
JP 2001506983-A/10.
                                                                                                                                                                  1 (bases 1 to 78)
Lees,A.M., Lees,R.S., Law,S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6355451-A 31 12-MAR-2002;
Location/Qualifiers
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AR199539
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                                                                                                                                                                                                                                                                Unclassified.
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/mol_type="genomic DNA"
/db_xref="taxon:6100"
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/mol_type="unassigned
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3 6355451.
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Sequence 31
AR374691
AR374691.1
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Unknown
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6632923-A 31 14-OCT-2003;
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/mol_type="genomic DNA"
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/mol_type="genomic"
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US-09-976-740-19

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BD056453
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         RS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.

Novel low density lipoprotein binding proteins and their use in
diagnosing and treating atherosclerosis
Patent: JP 2001506983-A 11 29-MAY-2001;
BOSTON HEART FOUNDATION INC
PN JP 2001506983-A/11
PD 29-MAY-2001
PF 26-NOV-1997 UP 1998524870
PR 27-NOV-1997 UP 60/031930,03-JUN-1997 US 60/048547 PI
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANLBAL A ARJONA PC
ASINSB/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC
C07H21/00, C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 (
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Low density liprotein binding proteins and the
and treating atherosclerosis
Patent: WO 0164874-A 31 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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1 (bases 1 to 78)
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Location/Qualifiers
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 20, 2003 this sequence version replaced gi:13938477.
Contact: MGC help desk
                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
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BC007384.2 GI:33988219
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AR199535
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                                                                                                                                                                                                                                                                                                             1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp
                    1 (bases 1 to 1208)
Lees,A.M., Lees,R.S., Law,S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6355451-A 16 12-MAR-2002;
Location/Qualifiers
                                                                                                                                                                                               Sequence 16
AR199535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row: g Column: 10.
                                                                                                                    Unc.
                                                                                                                                Unknown
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                                                                                                                                                                                                                            AR199535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SAM; Region: Sterile alpha motif. Widespread domain in signalling and nuclear proteins. In EPH-related tyrosine kinases, appears to mediate cell-initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="LOC90378 protein"
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TVMDVVEYFTEAGFPEQATAFQEQEIDGKSLLLMQRTDVLTGLSIRLGPALKIYEHHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In many cases "Guranto" /db_xref="CDD:smart00454"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="LOC90378"
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clone="IMAGE:3677194"
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hanie Rodrigues, Amy Sanchez and Michelle Whiting
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AR409322
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AR374687
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                                                                                     1 (bases 1 to 1208)
Lees,A.M., Lees,R.S., Law,S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
Patent: US 6632923-A 16 14-OCT-2003;
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Sequence 16 from
AR409322
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Score:

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/organism="unknown" /mol\_type="genomic DNA" Location/Qualifiers

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GI:40160110

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US-09-976-740-19 (1-15) x AR374687
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Sequence 16
AR374687
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,
Low density lipoprotein binding proteins a
diagnosing and treating atherosclerosis
patent: US 6605588-A 16 12-AUG-2003;
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Query Match:
Search completed: March 13, Job time : 231.827 secs
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Sequence 16 from Patent WO0164874.
AX239573
AX239573.1 GI:15797257
                                                             1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAsp 15
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Low density liprotein binding proteins and their use in diagnosing
and treating atherosclerosis
Patent: WO 0164874-A 16 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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|db_xref="taxon:9606"
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CGT2 1/USFT0_Sp0ol_p/US09976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N_Geneseq_29Jan04_QP/US09976740/runat_10032004_094547_19532/app_query.fasta_1.1898
-DB=N_Geneseq_29Jan04_QP/US09976740_SUFFIX=rng_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45_-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=sext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09976740 @CGN 1 1.596 @runat 10032004 094547 19532 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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  New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000; 2000US-00616289.
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diagnosis; vaccine; ss.
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RESULT 2
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   The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPs) of the invention (see AAB82797-820). LBPs are capable of binding to native and methylated low density lipoproteins (LDLs). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent
                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                  New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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                                                                                                                                                                                                                                             Disclosure; Page 9; 143pp; English.
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14-JUL-2000;
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AAV32838

AAV3288

AAV32
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03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human low density lipoprotein binding protein LBP-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions
                                                                                                                                                                                                                                                                                                                                                   26-NOV-1997;
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97US-0048547P.
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67. .99
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622. .651
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Nucleic related subjects

acid encoding low density lipoprotein binding proteins and vectors - transformed cells, proteins, and modulators of binding, for treatment and diagnosis of atherosclerosis and for identifying

1998-322455/28

AAW49041.

useful for treatment

at

Claim 9; Fig

16;

47pp; English

 $\mathbf{w} \mathbf{x}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{n}_{0} \mathbf{x}_{0}$ 

Sequence 1208 BP; 252 A; 368 C;

321 G; 266 T;

0 ₽

1 Other;

Sequence 1208

8P;

This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-2 (see AAW49041). It was isolated by screening human liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA clones (see AAW3804-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerotic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                            02-MAR-2000;
14-JUL-2000;
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                                                                                                                                                                                                                                                                                                 Human
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Example 4;
                                            P-PSDB;
                                                       WPI; 2001-565505/63.
                                                                        Lees AM,
                                                                                                                                       28-FEB-2001; 2001WO-US006356
                                                                                                                                                          07-SEP-2001
                                                                                                                                                                            WO200164874-A2
                                                                                                                                                                                                                                                                     atherosclerosis;
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                                                                                                                                                                                                                                                                    density lipoprotein binding protein 2; LBP-2; LDL; human;
erosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
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                                                                                                                                                                                                                                                                                                low density lipoprotein binding protein 2 (LBP-2) cDNA
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Fig 16;
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2000US-00616289.
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143pp;
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The present sequence is that of a partial cDNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were consisted from human foetal brain, liver and aorta cDNA libraries using crabbit LBP-2 cDNA as probe A full-length cDNA clone is given in active and are among claimed polymuclectides of the invention that encode convel polypeptides capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments can danalogues of them, as well as expression vectors, cells and methods cof atherosclerosis, methods for evaluating an agent for use in treating catherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed, pharmaceutical compositions, cc are also claimed polypeptide or nucleic acid, and vaccine compositions, or
  252 A; 368
  C; 321 G; 266
  구:
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  U; 1 Other;
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US-09-976-740-19 (1-15) Score: Query Match: Best Local Similarity: Percent Similarity: М о. 0.00852 82.00 100.00% 100.00% x AAH26494 (1-1208) Conservative: Mismatches: Indels: Length: Matches: Gaps: 1208 15 0

片 Ś RESULT 5 22 1 GluGluGluAspAspAspGluAspGluAspGluAspAsp GAAGAGGAAGATGATGAAGATGAAGATGAAGAAGATGAT 99 15

AAF21860

standard; DNA; 1336 ВP

27-MAR-2001 (first entry)

Human breast and ovarian cancer associated antigen gene SEQ ID 247.

nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds. Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;

Homo sapiens.

WO200055173-A1

08-MAR-2000; 2000WO-US005881

12-MAR-1999; 99US-0124270P

(HUMA-) HUMAN GENOME SCI INC

Rosen β Ruben SM;

WPI; 200 P-PSDB; 2000-611515/58. DB; AAB58957.

New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases. treatment

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RESULT 6
AAH26499
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New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                     WPI; 2001-565505/63
P-PSDB; AAB82806.
                                                                                                       Lees
                                                                                                                                                                       02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                        WO200164874-A2
                                                                                                                                                                                                                                                                                                                                                                       Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
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                                                                                                       Arjona AA;
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the coding region of the human gene (see CC also AAH26494) encoding novel human low density lipoprotein binding CC protein 2 (LBP-2, see AAB2206). The gene was isolated from a genomic DNA CC library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the CC present sequence differs from that predicted from a cDNA clone (see CAAB2203) in that it contains an additional 321 amino acids at its N-CC terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among CC claimed polymucleotides of the invention that encode novel polypeptides (capable of binding to native and methylated LDL. Also claimed are compared to them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for catherosclerosis, and methods for treating an agent for use in treating atherosclerosis, and methods for treating an agent for use in treating catherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions, or are also califed.
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          intron
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                                                                                                                                                                                                                                                                                                   Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
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/*tag=
4788. .
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4503.
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14-JUL-2000; 2000US-00616289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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P-PSDB; AAB82806.
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antimalarial; malaria;
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                                                                                                              Plasmodium falciparum
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                                                                                                                                                                  chromosome 2; human malaria parasite; protozoacide; infection; insecticide;
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The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). (I) and (CI) are useful for the development of vaccines against P. falciparum CC infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection CC of infection with P. falciparum. Furthermore, (I) (especially when they CC are rifins or secreted or membrane proteins) can aid the identification CC of drugs to treat or prevent P. falciparum infection, or they can be used CC to identify drug resistance in P. falciparum. Sequencing of the CC plasmodium chromosome 2 and the subsequent identification of proteins CC a process hampered by the complexity of the parasitic lifecycle, and CC provide new targets for vaccine and drug development. Parasite resistance CC of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA7027 and AAB18144 to AAB18352 CC represent nucleotide and protein sequences given in the present CC invention, but which are not specifically mentioned within the
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                                                                                                                                                                                             AAZ43754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection.
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(CARU/)
(GARD/)
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                                                                                                                                                  AAZ43754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2919
                                            treatment; ds.
                                                         NNX3; murine; cytostatic; marker; lung tumor; Hodgkin's disease;
                                                                                         Murine NNX3 cDNA
                                                                                                                     24-FEB-2000
                                                                                                                                                                               AAZ43754 standard;
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CARUCCI D.
GARDNER M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes two novel NNX3 proteins isolated from human and murine sources which have cytostatic activity. The NNX3 mRNA and/or protein is useful as a marker for lung tumors or Hodgkin's disease. The proteins form pharmaceutical compositions useful for treating lung tumors and/or Hodgkin's disease. Polynucleotide products of the invention form an assay for screening the expression of these nucleic acids. Antibodies raised against the proteins of the invention form an assay for detecting the proteins. The probes form an assay for detecting and/or amplifying NNX3 polynucleotides. The expression of NNX3 in humans and mice suggest that NNX3 is useful as a marker for lung tumors and Hodgkin's disease. This control of the protein facilitates therapies for these conditions. This
                                         antibody; imr
infertility;
                                                  Yeast; RRP3 gene; telomerase-associated protein; STR7; suppressor of telomeric repression-7; telomerase; ribonucleoprotein; telomere; tumour; pathogen; sperm; ovum; reporter gene; drug screeni antibody; immunoassay; antitumour; antiseptic; contraceptive;
                                                                                                                          RRP3 telomerase-associated protein gene
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                                                                                                                                                                                  AAT27052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therefore, the protein facilitates therapies for these conditions. I sequence encodes the murine NNX3 protein described in the method of
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Hodgkin's disease.
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Saccharomyces cerevisiae

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                                                  Hybridisation assay; genetic mapping; yelle way-unitary; metabolic protein identification; signal transduction pathway; metabolic promoter; termination sequence; ss.
                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reporter gene expression system linked to an expression-repressing telomere sequence, and binding compounds, e.g. antibodies, may be detected by complex formation with telomerase components. The products may be used as antitumour, antiseptic or contraceptive agents, in infertility diagnosis, or in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes combine with telomerase to repress telomere silencing of gene expression. Oligonucleotides from the sequence may be used to detect non-ciliate telomerase-associated genes, e.g. in tumour, pathogen, sperm or ownm cells. New telomerase-associated sequences may be detected by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae telomerase, a ribonucleoprotein required for telomere replication. Other genes associated with telomerase are given in (telomerase RNA template gene) and AAT27046-50 (other STR genes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel telomerase associated polypeptide (s) and related nucleic acid useful for detecting e.g. tumour cells or pathogens.
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28-APR-1995;
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Garcia CA,
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Kricker M,
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Ledford BL, Woessner
Davis KR, Allen K,
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New Arabidopsis thaliana nucleic acid for identifying homologous producing compositions that modulate the expression or function cencoded protein, and mapping functional regions of protein.

Yu Y;
JP, Haas W
Hoffman N;

ΨĎ,

Claim 1; SEQ ID NO 559; 49pp + Sequence Listing; English

Comprising a sequence capable of hybridising under strangent conditions comprising a sequence capable of hybridising under strangent conditions considered from any one of 998 sequences (ABN99231-ABN99231). CC given in the specification or its fragment. A polypeptide (II) encoded by CC (II), a transgent plant (III) comprising an exogenous nucleic acid or a CC genetically modified cell (IV) comprising an exogenous nucleic acid, is cuseful for screening a candidate agent for its biological effect. (I) is CC useful for screening a candidate agent for its biological effect. (I) is compositions that modulate the expression or function of its encoded CC protein, mapping functional regions of the protein and in studying CC associated physiological pathways. (I) is also useful for the genetic composition of cells, particularly plant cells. (I) is also useful in Screening assays of various plant strains to determine the strains that CC are best capable of withstanding a particular disease or environmental CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC pathways. The screened agents are useful for screening of biologically active capable of proteins are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening CC programs to identify agents that mimic or enhance the action of tolerance to environmental stress. (I) is also useful for composition of proteins of interest, for establishing the extent to which capation of particular plant, for identifying other mediators that may induce tolerance to environmental stress. (I) is also useful for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress, for identifying factors involved in the study of genetic function and regulation, of the printed constitution of the gene or gene products. CC walve. (IV) is useful in the study of genetic function and regulation, for alteration of the printed specification, but was obtained in electronic f The invention relates to an Arabidopsis thaliana nucleic acid (I)

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RESULT 13
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The invention relates to constructing (MI) a strain of diploid fungal collisin which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an composition of the selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter. (MI) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal colls in which both alleles of a gene are modified. The diploid fungal colls having both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus cand for identifying a therapeutic agent for treatment of a mammalian compound catabolism, biosynthetic, transporter, transcriptional, carbon compound catabolism, biosynthetic, transporter, transcriptional, carbon compound catabolism, biosynthetic, transporter, transcriptional.

Claim

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signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; gene; ss.
                                                                                                                                                                                 Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
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20-FEB-2001; 2001US-00792024
22-AUG-2001; 2001US-0314050P
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Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors o inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for cana there.
                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000EP-00870318.
04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                               Claim
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Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-2001; 2001WO-EP015398
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINNATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -DOCALIGN=10 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MCDE=LOCAL -CUTINNT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_WMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOD=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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4: /cgm2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgm2_6/ptodata/2/ina/Bottoftoms.seq:*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 12, 2004, 20:05:17 ; Search time 5.08568 Seconds (without alignments) 1636.805 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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82
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78
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12425
1514
15425
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US-08-979-608A-30
US-09-517-849-30
US-09-516-289-30
US-08-979-608A-31
US-09-517-849-31
US-09-517-849-31
US-09-517-849-16
US-09-517-849-16
US-09-616-289-16
US-09-616-289-16
US-09-616-289-50
US-09-616-289-50
US-09-616-289-50
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Sequence 30, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 45, Appl
Sequence 50, Appl
Sequence 50, Appl
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US-08-979-608A-30
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equence 20, App	equence 1, Appl	equence 1, Appl	equence 1, Appl	equence 816, Ap	equence 66, App	equence 15, App	equence 9, Appl	equence 9, 1	equence 9, Appl	equence 3, Appl	equence 3, Appl	equence 3, Appl	equence 3, Appl	equence 1, Appl	equence 1, Appl	equence 55, App	equence 1, Appl	equence 1, Appl	equence 4, Appl	equence 1415, A	equence 3, Appl	equence 31,	equence 32, App	equence 25, App	equence 32, App	equence 25, App	equence 32, App	equence 25, App	equence 22, App	equence 66, App	quenc	equence 27, App

#### ALIGNMENTS

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Sequence 30. Application US/08979608A
Patent No. 6355431

GENERAL INFORMATION:
Lees, Robert S.
Law, Simon M.
APPLICANT: Lees, Ann M.
ILees, Robert S.
Law, Simon M.
APPLICANT: Lees, Ann M.
ITITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING /
BINDING SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COMPUTER READABLE FORM:
MEDIUM TYPE: DIskette
COMPUTER READABLE FORM:
MEDIUM TYPE: DIskette
COMPUTER: IMPCOMPALIANCE
COMPUTER: 18 COMPALIANCE
COMPUTER: 18 COMPAL
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-517-849-30
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: SEQUENCE 45 base pairs TYPE: nucleic acid
                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 10797-003001
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: USA
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09517849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Law, Simon W.
Arjona, Anibal A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lees, Robert S.
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Matches:
Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
US-09-616-289-30
; Sequence 31, Application patent No. 6353451 ; GENERAL INFORMATION: APPLICANT: Lees, F. Lees, F.
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence LOCATION: 1...45
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear FEATURE:
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10. 663292
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                                                                                                                                       44
                                                                                                                                                         1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp
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                                                                                                                                       Application US/09616289
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 Ann M.
Robert S.
                                                                   US/08979608A
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 5
(WS-09-517-849-31)
(Sequence 31, Application US/09517849)
Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-976-740-19 (1-15) x US-08-979-608A-31 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NUMBER: MOST 10:1016
ATTORNEY/AGENT INFORMATION:
                             APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nyers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
                                                                                                                                                                                                                                                                                                                               LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence LOCATION: 1...78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: AIOna, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BIN TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNO TITLE OF INVENTION: APTEROSCLEROSIS
FILE REFERENCE: 10797-004001
CUURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/99,608
PRIOR FILING DATE: 1907-11-26
PRIOR APPLICATION NUMBER: US 60/979,608
PRIOR APPLICATION NUMBER: US 60/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
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Query Match:
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US-09-616-289-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MYSE'S, LOUIS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 1079
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-5076
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 66329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-MOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAsp 15
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 1...78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
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Matches:
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Indels:
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DB:
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Best Local Similarity:
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Pred. No.:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-616-289-31
; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-08-979-608A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application Patent No. 6355451
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 31
                                                                                                                                                       TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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                                                                      FEATURE:
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78
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                                                                                                  LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 APPLICATION DATA:
                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
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                                                                                       TOPOLOGY: linear
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                                                    Coding Sequence
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Sequence
PATENT NO. 6605550
PATENT NO. 6605500

APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
Arjona, Anibal A.
BINDING PROTEINS AND THEIR USES IN I
TREATING ATHEROSCLEROSIS
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US-09-517-849-16
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Best Local Similarity:
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Pred. No.:
Query Match:
DB:
                            Percent Similarity:
Best Local Similarity:
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                                                                         Pred. No.:
                                                                                       Alignment Scores:
                                                                                                                    US-09-517-849-16
                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                               LOCATION: 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                           NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                          LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
                                                                                                                                                              NAME/KEY:
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                                           Length:
Matches:
Conservative:
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Indels:
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: ALW, Simon W.

APPLICANT: ALY, Simon W.

APPLICANT: ALY, Simon W.

APPLICANT: ALY, SIMON W.

TITLE OF INVENTION: MOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 1997-11-26
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US-09-616-289-45
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; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-09-616-289-16
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Best Local Similarity:
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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR TILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR PPLICATION NUMBER: US 60/031,930
PRIOR PPLICATION NUMBER: US 60/031,930
PRIOR PPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1996-01-27
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGIH: 1208
                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6632923
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                     45, Appl
o. 663292
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Matches:
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lew, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Anibal A.

APPLICATION: ANIBAL A.

APPLICATION: ANIBAL A.

ITITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND THILE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND THEIR DEFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR PRIOR AND THE STANDARD S
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                     US-09-976-740-19 (1-15)
                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                           US-09-616-289-50
                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5
Patent No.
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TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 12425
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
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                                           GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp
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Indels:
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US-08-938-534-27
; Sequence 27, Application US/08938534
; Patent No. 5916752
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US-08-431-080-27
; Sequence 27, A
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DB:
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Best Local Similarity:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION: Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Co
                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (713) 789-267
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, VeCURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
                                                                    APPLICANT: Gottschling, Daniel E. APPLICANT: Singer, Miriam S. TITLE OP INVENTION: Telomerase CONUMBER OF SEQUENCES: 32
                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Houston
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P.O. Box 4433
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS/ASCII
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89.02%
                                                                      Telomerase Compositions and Methods:
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4599 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: PARKER, DAVID L.
REGISTION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: October 20, 1994 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,294
FILING DATE: 30-Jun-1999
CLASSIFICATION: UNKnown>
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                          Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods NUMBER OF SEQUENCES: 32
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1231 GAAGAAGAAGATGATGACGAAGACGACGACGATGATGAT 1275
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gottschling, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
                                                                                                                                                                                                                     CITY: Houston
STATE: TEXAS
                                                                                                                                                                                                COUNTRY: UNITED STATES OF AMERICA
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713) 789-2679
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                                                                                       Version #1.30
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Sequence 66, Application US/09220132

Sequence 66, Application US/09220132

Patent No. 6506607

GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 07334-074001

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT FILING DATE: 1998-12-23

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1997-12-24

NUMBER: OF SEQ ID NOS: 191

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 66

LENGTH: 2736

TYPE: DNA
ORGANISM: Homo sapiens

US-09-220-132-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/431,080
FILING DATE: FULING DATE: FULING DATE: 
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHAX: (713) 789-2679
TELEY X: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4599 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: 11near
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-345-294-27
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US-09-220-132-66
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                            US-09-976-740-19 (1-15) x US-09-220-132-66 (1-2736)
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1325 GAAGAAGAGGATGAGGATGAGGATGAGGATGAAGATGAGGAT 1369
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                         1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: March 13, 2004, 04:06:22 Job time : 9.08568 secs

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-MODEL-frame+ p2n.model -DEV=xlp
-MODEL-frame+ p2n.model -DEV=xlp
-C2-/Ggn2 _L/USPTO_Spool_p_/US09976740/runat 10032004_094549_19588/app_query.fasta_1.1898
-DB=Published_Applications_NA -QFMT=fastap_-SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS_bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US09976740 @CGN 1 1712 @runat 10032004 994549 19588
-NCFU=6 -TCPU=3 -NO_MMAP -LARGEQUERY -NUST SCORES=0 -MAIT -DSPBLOCK=100 -
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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score greater than
and is derived by
      Score
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                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
                                                                                                                                                   is the number of results predicted by chance to have ater than or equal to the score of the result being purived by analysis of the total score distribution.
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Query
Match Length
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Copyright (c) 1993 - 2004
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9 US-09-976-740-30
12 US-10-671-242-30
13 US-10-616-187-30
14 US-10-616-187-30
15 US-10-616-187-30
16 US-09-976-740-31
17 US-10-616-187-31
18 US-10-616-187-31
19 US-09-976-740-16
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10 US-10-616-187-16
11 US-10-616-187-16
12 US-10-616-187-16
13 US-10-023-529-16
14 US-10-102-8076-247
16 US-10-616-187-16
17 US-09-976-740-45
18 US-10-616-187-16
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10 US-10-616-187-16
11 US-10-616-187-16
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13 US-10-023-529-45
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19 US-09-976-740-45
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19 US-09-976-740-59
10 US-10-616-187-50
11 US-10-616-187-50
12 US-10-616-187-50
13 US-10-023-523-50
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19 US-09-976-740-45
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19 US-09-976-740-45
10 US-10-032-585-6386
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10 US-10-032-585-6386
10 US-10-035-7833-7014
15 US-10-035-7833-7014
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 16, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 50, Appl
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## ALIGNMENTS

Application US/09962055

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RESULT 1
US-09-962-055-30
; Sequence 30, Application U
; Patent No. US20020052033A1
; GENERAL INFORMATION:
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
                                                                                                                           NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                    APPLICANT: Lees, Ann M.
Lees, Robert
                                                                                                                                                                                                                                                                 TITLE OF
                                                                                                                                                           Lees, Robert L.
Law, Simon W.
Arjona, Anibal A.
Arjona, NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
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; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-740-30
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-976-740-30
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
                                                            SEQ ID NO 30
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CURRENT APPLICATION UNMER: US/09/962,055
APPLICATION UNMER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION UNMER: 08/979,608
APPLICATION UNMER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEPHAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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LOCATION:
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2007-09-24
PRIOR APPLICATION NUMBER: US/99/616,289
PRIOR APPLICATION NUMBER: US/99/616,289
PRIOR APPLICATION NUMBER: US/99/517,849
PRIOR APPLICATION NUMBER: US/99/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-023-529-30
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Best Local Similarity:
Query Match:
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Query Match:
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                                                                                                                                Sequence 30, Application US/10023529
Publication No. US20020129388A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 30
LENGTH: 45
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                              APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
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10. US20040040049A1
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Matches:
Conservative:
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                          AND TREATING
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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CURRENT FILING DATE: 2001-12-17
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Aziona, Anibal A.
ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVEL LOW DENSITY SIMONOSING AND
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2007-012-17
PRIOR APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR DE 05/517,849
PRIO
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US-10-023-523-30
JS-10-023-523-30
Sequence 30, Application US/10023523
Publication US20020152485A1
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; ORGANISM: Homo sapiens
US-10-023-529-30
                                                                                                                                                                                                                                                       LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-523-30
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 30
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                    Length:
Matches:
Conservative:
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Percent Similarity:

ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston

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Sequence 30, Application US/10616187

| Sequence 30, Application US/10616187
| Publication No. US20040013668A1
| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M.
| APPLICANT: Lees, Robert S.
| APPLICANT: Lees, Robert S.
| APPLICANT: Law, Simon W.
| APPLICANT: Law, Simon W.
| APPLICANT: Arjona, Anibal A.
| APPLICANTON: ANTHEROSCIEROSIS
| FILLE REFERENCE: 10797-004001
| CURRENT APPLICATION NUMBER: US/10/616,187
| CURRENT FILING DATE: 2003-07-09
| PRIOR APPLICATION NUMBER: US 09/517,849
| PRIOR A
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Best Local Similarity:
Query Match:
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US-10-616-187-30
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DB:
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US-09-962-055-31
j Sequence 31, Application US/09962055
j Patent No. US20020052033A1
j GENERAL INFORMATION:
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                                                       APPLICANT: Lees, Ann M.
Lees, Robert S.
Lees, Robert S.
Law, Simon W.
Law, Simon W.
Arjona, Anibal A.
Arjona, Anibal A.
BINDING PROTEINS AND THEIR USES
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAsp
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APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US/09/97,608

PRIOR APPLICATION NUMBER: US/09/9,608

PRIOR PILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US/09/9,608

PRIOR FILING DATE: 1997-06-03

PRIOR FILING DATE: 1997-06-03

PRIOR FILING DATE: 1997-06-03
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Best Local Similarity:
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REGISTRATION NUMBER: 35,965
REFERRNICS/NOKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION NUMBER: US/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US/979,608
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
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COUNTRY: USA
ZIF: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1907-11-26
PRIOR APPLICATION NUMBER: US/09/99,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US/09/031,930
PRIOR FILING DATE: 1997-66-03
PRIOR PILING DATE: 1997-66-03
PRIOR PILING DATE: 1997-06-03
                                                        RESULT 10
US-10-023-529-31
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Best Local Similarity:
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SSETIWARE: FastSEQ for Windows Version
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
ORGANIZM: Homo sapiens
US-10-671-242-31
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-976-740-31
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; Publication No. US20
; GENERAL INFORMATION
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Sequence 31, Application US/10023529 Publication No. US20020129388A1 GENERAL INFORMATION:
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No.:
                                                                                                                                    1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAsp
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APPLICANT: LEED, NOVEL LOW APPLICANT: LAW, SIMON W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/9/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEO for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
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APPLICANI: ATJONA, ANTIBAI A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BIN

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNO

TITLE OF INVENTION: ATHEROSCLEROSIS

FILLE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,529

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR APPLICATION NUMBER: 09/517,849

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1996-11-27

PRIOR PRIOR DATE: 1910-11-27

PRIOR FILING DATE: 1910-11-27

PRIOR PRIOR PRIOR DATE: 1910-11-27

PRIOR PRIOR DATE: 1910-11-27

PRIOR FILING DATE: 1910-11-27
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Best Local Similarity:
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Pred. No.:
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SOFTWARE: Fast
SEQ ID NO 31
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Publication No. US20020152485A1
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TYPE: DNA
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TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 13
US-09-962-055-16
, Sequence 16, Application US/09962055
, Patent NO. US20020052033A1
, GENERAL INFORMATION:
, APPLICANT: Lees, Ann M.
, Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/616,289

PRIOR APPLICATION NUMBER: US 09/9517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR PILING DATE: 1997-11-26

PRIOR PILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR PILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                              Percent Similarity:
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; ORGANISM: Homo sapiens
US-10-616-187-31
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                                                                                                                                                                                                                                                        US-09-976-740-19 (1-15) x US-10-616-187-31 (1-78)
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 31
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No
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Matches:
Conservative:
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TITLE OF

Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

AND

```
Sequence 16. Application US/09976740

Publication No. US20020194633A1

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND

TITLE OF INVENTION: APPLEXCELEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/9/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                   US-09-976-740-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1208 base pairs
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Arjona, Anibal A.
FITTLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
FITTLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
FITTLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
    Query Match:
                     Percent Similarity:
Best Local Similarity:
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                                                                                                    Alignment Scores:
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Best Local Similarity:
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Pred. No.:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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APPLICANT:
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                                                                                                                                                              LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No.
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
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NAME/KEY: CDS
LOCATION: (1)...(651)
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Law, Simon W.
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No. US20040040049A1
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Matches:
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망	80	US-09-9	DB:
22 GAAGAGGAAGATGATGATGAAGATGAAGATGAAGATGAT 66	1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15	US-09-976-740-19 (1-15) x US-10-671-242-16 (1-1208)	12 Gaps: 0

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-Q=/-Ggn2 1/USPTO, Spool p./US09976740/runat 10032004 094548 19551/app_query.fasta_1.1898
-DB=8ST -QPMT=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -NODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR-US09976740 @CGN 1 1 10232 @runat 10032004 094548 19551 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCKE100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOD=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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   US-09-976-740-19
82
1 EEEEDDDEDEDEEDD 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    March 12, 2004, 19:55:37; Search time 226.799 Seconds (without alignments)
1975.018 Million cell updates/sec
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em htc: *
gb est1: *
gb est2: *
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gb est5: *
em estfun: *
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em_gss_mam: *
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em_gss_pro: *
em_gss_pro: *
em_gss_vrl: *
gb_gssl: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5
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# 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

00044444 00040840	1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2	C 5 4 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
8 8 8 8 8 8 8 8 8 N N N N N N N N			Score
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10 10 10 10	90 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	10 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	DB.
570 570 570 570 579	X60	807448 E50487 742585 7481527 765474 100456 806888 806888 810871 7166034 710106	ID
269536 60118475 597252 UITE DXO 257093 60110802 257093 60110802 256679 wf23ell.x 23580 qa50bll.x 26488 wp02ell.x 257956 7f73all.	## 0007 o CV4+CV815219 o C05b08 ## 15019 o C05b08 ## 15019 o C074+CV7 ## 15019 o C037b0 ## 15018 o C03	807448 nv65b12.s 807448 17 hz3395. 481545 aa35906.s 742585 wg55907.x 742585 wg55907.x 806888 oc32906.s	Description

#### ALIGNMENTS

RESULT 1

AA807448	
LOCUS	AA807448 171 bp mRNA linear EST 18-FEB-1998
DEFINITION	nv65b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234655 3'
	similar to contains element MER22 repetitive element ;, mRNA
	sequence.
ACCESSION	AA807448
VERSION	AA807448.1 GI:2877024
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                 BE504871
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
COMMENT
                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                   KEYWORDS
                                                                                                                                   VERSION
                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 200)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                   Homo
                                                                                                                                                                                   BE504871 200 bp mRNA linear EST 04-AUG hz33g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3209816 similar to contains element TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1069 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
(1997)
(Inpublished (1997)
(Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Iissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allmartis M.D., Gerald Marti, M.D.
(CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1069 Std Error: 0.00
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                   Homo
                                                                                                                                   BE504871.1
                                                                                                                                                                                                                                                                                      GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
                                                                                                 sapiens (human)
                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'tissue_type="germinal center B
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:1234655"
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                                                                                                                                     GI:9707279
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Matches:
Conservative:
Mismatches:
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JOURNAL
COMMENT
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AA481545
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Best Local Similarity:
Query Match:
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                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (Dases 1 to 204)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                  aa35g06.s1 NCI_CGAP_GCB1
similar to contains eleme
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DNA Sequencing by: Mashington University Genome Sequencing (
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
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Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., E
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares,
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Contact: Robert Strausberg, Ph.D.
Bonaldo,
                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                            Homo sapiens
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NCI_CGAP GC6"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP GC4 was prepared, and
s circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subbractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257996-1258631, 14699064-1470993, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3209816"
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                                                           David Allman,
                     M. Fatima
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 901 Std Error: 0.00
Seg primer: -40Up from Gibco
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AI742585.1 GI:5110873
EST.
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Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 203.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                  Unpublished (1997)
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quality sequence stop:
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//clone lib="NCI CGAP GCGAP GCGAP GCGAP GCDAP
//clone lib="NCI CGAP GCGAP G
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/lab_host="DH10B"
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mol_type="mRNA"
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'db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 GAAGAGGAAGATGATGAAGATGAAGATGAAGAAGATGAT
                                                                                                                                                                                                                                                                                                                                                         aa35e06.s1 
similar to
                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
Bonaldo, Ph.D.
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 244)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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NCI_CGAP_GCB1 Homo sa
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sapiens cDNA clone IMAGE:815266
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                                Sequencing Center information can be
                                                                                                                      David Allman,
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Possible reversed clone: polyT not found Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 243.

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SOURCE
ORGANISM
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AA765474
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
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                                           source
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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DMA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1136 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 269.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHA/55474 271 bp mRNA linear EST 08-FEB-1998 oa03d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303873 3' similar to contains Alu repetitive element;contains element MER22_repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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//Glone lib="WCI_CGAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_GCBAP_G
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|lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 GAAGAGGAAGATGATGATGAAGATGAAGATGAAGATGAT 126
            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-HN0054-
070301-002-g904&t3=2001-03.-07&t4=1)
Seq_primer: puc 18 forward
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Ragai,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                            sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97
                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI004562 274 bp mRNA linear MR4-HN0054-070301-002-g04 HN0054 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                        10737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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quality sequence start: 39
                                                                                                                                            +55-11-2707001
                                                                                                                                                                 +55-11-2704922
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
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밁 Ś Best Score:

RESULT 7

VERSION KEYWORDS

SOURCE

REFERENCE

AUTHORS

COMMENT

JOURNAL MEDLINE PUBMED

TITLE

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ACCESSION
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ORGANISM
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AA806888
LOCUS
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
DORALISTARY Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA806888 275 bp mRNA linear EST 07-APR-1998 oc32g08.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1151450 3' similar to contains element TAR1 repetitive element ;, mRNA
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                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 275)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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/note="Organ: head normal; Vector: pucl8; Site_1: Smal;
/note="Organ: head normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pull svector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                /organism="Homo sapiens"
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/lab host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                                                        clone="IMAGE:1351450"
tissue_type="germinal center B cell"
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82.00
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Matches:
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0
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                                                                                                                                                                                                                                                                                                           Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                      David Allman,
                                                                                                                                                                                                                                                                                                                                                                                              M. Fatima
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ORIGIN

#### Percent Similarity: Best Local Similarity: Query Match: DB: JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT 9 AA810871 밁 á US-09-976-740-19 (1-15) x AA806888 (1-275) FEATURES Score: Alignment TITLE No.: source Scores: Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 278) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), AA810871 AA810871 278 bp mRNA linear EST 19-FEB-1998 ob64g05.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1336184 3' similar to contains element PTR7 repetitive element ; mRNA Tumor Gene Index Unpublished (1997) AA810871.1 GI:2880482 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" clone="IMAGE:1336184" 0.43 82.00 100.00% 100.00% 100.00% Length: Matches: Conservative: Mismatches: Indels: Gaps: 275 0 0 15 David Allman, M. Fatima

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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not IT, Site\_2: Eco RI; 1st strand was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-),

CDNA

/tissue\_type="germinal center B cell"
/lab\_host="DH10B"

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

(Pharmacia), digested with Not I and cloned into tand Eco RI sites of the modified py73 vector. Lib went through one round of normalization, and was constructed by Bento Scares and M. Fatima Bonaldo.  0.435   Length: 278   278   82.00   Matches: 0   150.00%   Matches: 0   100.00%   Matches: 0   10	FEATURES FEATURES FEATURES	JOURNAL UN COMMENT Em Ti Ph	MARREFERENCE 1 AUTHORS NC TITLE NA	S ON CON	82 SULT 10 .766034 AP	US-09-976-740- Qy 1	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similari Query Match: DB:	ORIGIN
ph.D., David All ph.D., David All ph.D., M. Fatima  ph.D., M. Fatima  ph.D., M. Fatima  ph.D., M. Fatima  clome informatio.  ph.D., M. Fatima  clome sequencing  mation informatio.  ph.D., M. Fatim  conglished for string (CD204.)  consider  consider  colls enriched for colls consider  colls enriched for colls co	UNA Library Arrayed by NA Sequencing by: Wash NA Sequencing by: Wash Na Sequencing by: Wash llone distribution: NCI wand through the I.M.A. wand through the I.M.A. wand through the I.M.A. wand through the I.M.A. was prepared the year "Ball in the "NCI / Load to Man Sequence st Location/Qualif 1. 284 / Organism="Homo / Mol Type="maNA / Ab xref="taxon / Clone="IMAGB: I.T / Lissue_type="g / lab host="DH10 / Clone I lib="NCIO" / Otone I lib="NCIO" / Note="Tector: yolylinker; Sit was prepared fr was prepared for germinal center provided by Dr. (NCI) and Dr. G primed with a N	Unpublished (1997) Contact: Robert Strausbe Email: cgapbs-remail.nih Tissue Procurement: Loui Ph.D., Gerald Marti, M.D CDNA Library Preparatio Bonaldo, Ph.D.	theria; Printo 284) p://www.ncbi cer Institut	b09.s1 NCI CGAP lar to contains ence. 6034.1 GI:2817: 8034.1 GI:2817: sapiens (human)	2 GAAGAGGAAGAAGATGATGATG 2 GAAGAGGAAGAAGATGATGATGATGATGATGATGATGATG	19 (1-15) x AA810871 ( GluGluGluGluAspAspAspG	ty:	[5'-TGTTACCAAP(T) [5'-TGTTACCAAP(T) ]. DOUble-stran (Pharmacia), dil (Pharmacia), dil and Eco RI site went through on constructed by
ary I	Henome Sequencing Cerution information caution information caution information calls enriched for cells enriched for cells enriched for colls enriched for cells enriched for orting (CDD-, IgD-), IgD-), IGI), Dr. David Allman cDNA synthesis was timer	Ph.D., Davi	; Catarrhini; Hominidae; Homo. .nih.gov/ncicgap. ancer Genome Anatomy Project (CG	o sapiens CDNA clone IMAGE:13950 MER22 repetitive element ;, mRNA	126 ar EST 08-FEB		lve:	GAAGIGGGAGGGCGCGCTCATTTTTTTTTTTTTTTTTTTGAAGIGGGCGCGCGCTCATTTTTTTTTT

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 11 BF194967 LOCUS Percent Similarity:
Best Local Similarity:
Query Match: 밁 FEATURES COMMENT S DEFINITION  $US-09-976-740-19 (1-15) \times AA766034$ Alignment Scores: Pred. No.: JOURNAL source Bukaryota; Metazoa; Chordata; Craniata; vertebrata; butervoccom, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 302)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Micha
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov. BF194967 302 bp mRNA linear EST 03-NOV-2000 7091b05.x1 NCI\_CGAP\_Ov18 Homo sapiens cDNA clone IMAGE:3643712 3' similar to contains element TAR1 TAR1 repetitive element ;, mRNA Tumor Gene Index Unpublished (1997) BF194967 BF194967.1 GI:11081346 Homo sapiens Homo sapiens location/Qualifiers 100.00% 100.00% 100.00% 0.445 (human) Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. (1-284)Mismatches: Indels: Gaps: Length:
Matches:
Conservative: 8 H 0 0 0 0 0 4 Michael эd

Alignment Scores:

Pred. No.:

0.474 82.00

Length: Matches:

302 15

mRNA sequence.

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AI470106
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                                                                              US-09-976-740-19 (1-15) x AI470106 (1-322)
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Best Local Similarity:
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1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI470106 322 bp mRNA linear EST 14-APR-1999 tj90g09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148832_3' similar to contains TAR1.b2 PTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 387 Std Error: 0.00 Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                 /lab host="DH10B"
/clone lib="Soares NSF F8 9W OT PA P S1"
/clone lib="Soares NSF F8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
30384-310919, 333208-325895 Soares NbHSP pool 1:
145032-147335, 147720-148103, 14872-149255, 15002 -
150407, 151176-152327 Soares NbHFP pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
758280-760583, 772104-77407 Soares NbHPA pool 1:
758280-760583, 772104-77407 Soares NbHPA pool 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                            RESULT 14
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BF806978
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Eriones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
AA815219 326 bp mR1 oc05504.s1 NCI_CGAP_GCB1 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-CI0151-091100-522-a05&t3=2000-11-09&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                        GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp 15
                                                                                                                                         Nat1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=Torgan: colon ins; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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RESULT 15
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           sequence.
BF941758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 326)
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AA815219
AA815219.1 GI:2884815
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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GI:12359078
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Search completed: March 13, Job time: 232.799 secs

2004, 04:01:36

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KEYWORDS
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159 GAAGAGGAAGATGATGAAGATGAAGATGAAGAAGATGAT 203
                    1 GluGluGluAspAspAspGluAspGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
1 (bases 1 to 345)
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Location/Qualifiers
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Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                      /mol_type="mRNA"
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Command line parameters:

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-MODEL-frame+ p2n.model -DEV=xlp
-Q=/Ggn2_1/USPTO_Spool_p/US09976740/runat_10032004_094548_19540/app_query.fasta_1.1898
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              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2004 Compugen Ltd.
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35: em_htg_mus:*
36: em_htg_mam:*
37: em_htg_mam:*
38: em_htg_vrt:*
38: em_htg_o_hum:*
40: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their
diagnosing and treating atherosclerosis
Patent: US 6605588-A 31 12-AUG-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their use
diagnosing and treating atherosclerosis
Patent: US 635451-A 31 12-MAK-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                  Unknown
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Lees, A.M., Lees, R.S.,
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/mol_type="genomic
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/mol_type="unassigned
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SOURCE
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Sequence 31
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                                                                                                                                          Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density liprotein binding proteins and the
and treating atherosclerosis
Patent: WO 0164874-A 31 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and their
diagnosing and treating atheroselerosis
Patent: US 6632923-A 31 14-OCT-2003;
                                                                                                                                                                                                                                                     Homo sapiens (human)
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Mammalia;
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/mol_type="unassigned DN/
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/mol_type="genomic DNA"
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Novel low density lipoprotein binding proteins and their use in
diagnosting and treating atherosclerosis

AL Patent: JP 2001506983-A 11 29-MAY-2001;
BOSTON HEART FOUNDATION INC

PN JP 2001506983-A/11

PD 29-MAY-2001

PF 26-NOV-1997 JP 1998524870

PF 26-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547 PI

ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC

A61X38/04, A61X38/17, A61X39/00, A61X48/00, A61X49/00, A61X51/08, PC

CO7H21/00,
CC7H21/00, CC7K1/4/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC

Strandedness: Single;
CC Topology: Linear;
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IMAGE:3677194),
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/mol_type="genomic DNA"
/db_xref="taxon:6100"
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      GI:33988219
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Uordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bossk, S.A., McDewan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sonchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Mazra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Mal.

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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on Aug 20, 2003 this sequence version replaced gi:13938477.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row. g Column: 10.

Location/Qualifiers
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Direct Submission

Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Submitted (01-MAY-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6355451-A 16 12-MAR-2002;
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                          GAAGTGCCCGAGAGTGAC
                                             GluValProGluSerAsp
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                                                                                              GluGluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6605588-A 16 12-AUG-2003;
Location/Qualifiers
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Sequence 16 from patent US 66
AR409322
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Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density lipoprotein binding proteins and t
diagnosing and treating atherosclerosis
Patent: US 6632923-A 16 14-OCT-2003;
Location/Qualifiers
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BD056449.1 GI:22602055
JP 2001506983-A/7.
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Aequoreidae; Aequorea.

(bases 1 to 1208)
Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
Novel low density lipoprotein binding proteins
diagnosing and treating atherosclerosis
Patent: JP 2001506983-A 7 29-WAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
Low density liprotein binding proteins and their use in diagnosing
and treating atherosclerosis
Patent: WO 0164874-A 16 07-SEP-2001;
Boston Heart Foundation, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 from Patent AX239573
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                                                                                                      Aequorea victoria
                                                                                                                  Aequorea victoria
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                              their use
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; Homo.
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US-09-976-740-20 (1-26) x BD056449
                                            Homo sapiens (human)

ISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CE (bases 1 to 1470)

CE Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,X.S., Krzyvinski,M.I., Skaiska,U., Smailus,D.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA semences
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PN JP 2001506983-A/7
PD 29-MAY-2001
PF 26-NOV-1997 JP 1998524870
PF 26-NOV-1996 US 60/031930,03-JUN-1997 US 60/048547
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC
A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08,
C07H21/00,
C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/5
PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/5
Strandedness: Single;
CC Topology: Linear;
FH Key Linear;
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   human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone
IMAGE:3943601), partial cds.
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/mol_type="genomic DNA"
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Alignment Scores: Pred. No.:
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gr
Series: IRAL Plate: 15 Row: m Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:22539615.
Contact: MGC help desk
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                                                                                                                              /gene="LOC90378"
/note="SAM; Region: Sterile alpha motif. Widespread domain in signalling and nuclear proteins. In EPH-related in signalling and nuclear proteins. In EPH-related cyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="LocusID:90378"
/translation="GaarpvoslrevvrylggsggaggrltrgrvQgllreeaaargrltrtrgrvQgllreeaaargrlertrgrvQgllreeaaargrlertrgrvQgllreedbeddebeddebeddes Ertrlgalalprgdpegrapapaagarerskrggeervlekeeeebddebedbeddebeddes Estrvqesdreaagardpolnoergpgsakervkewtpcophqqqdbegropapaggrr vssmaamskeggtasvatgpdspspvplppgkpalpgaddtpfgcppgrkekpsdpvewtymdvveyfteagfpegatafqeqeldgkslllmqrtdvltglstrlgpalktyehh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                IKVLQQGHFEDDDPDGFLG"
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/clone lib="NIH MGC 7"
lab_host="DH10B-R"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                              1614 bp
Sequence 45 from Patent WO0164874.
AX239602
                                                                                                                                                                                                                                                                                                            1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20
and treating atherosclerosis Patent: WO 0164874-A 45 07-SEP-2001; Boston Heart Foundation, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis Patent: US 6632923-A 45 14-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45
AR409337
                                                                                                   Eukaryota;
                                                                                                                Homo sapiens
                                                                                                                                                    AX239602.1 GI:15797275
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Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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                                                Lees,A.M., Lees,R.S., Law,S.W. and Arjo
                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
                                                                                        Mammalia;
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from patent US 6632923.
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                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Submitted (30-CCT-2003) Harvard-MIT Division of Health Sciences and Technology, Boston Heart Foundation, 139 Main Street, Cambridge, MA
                                                                                                                                                                                                             2 (bases 1 to 1617)
Deconinck, A.E., Law,
                                                                                                                                                                                                                                                      Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S. Atherin, a newly identified LDL-binding protein in human atherosclerotic lesions
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1617)
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#### ORIGIN

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Search completed: March 13, 2004, 00:35:26 Job time: 396.901 secs

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Result
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2: geneseqn1980s:*
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## ALIGNMENTS

RESULT 1
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ID AAH2
XX AAH2
XX AAH2
XX Low
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XX ATI
PF 28-I
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PR 114-I
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PR 14-I
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PR 14-I
XX XX ATI
PR 02-MAR-2000; 2000US-00517849. 14-JUL-2000; 2000US-00616289. Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine; ss. AAH26503; AAH26503 standard; DNA; WPI; 2001-565505/63. 28-FEB-2001; 2001WO-US006356. 07-SEP-2001. WO200164874-A2 Mammalia. Low density lipoprotein binding protein (LBP) polynucleotide 12-NOV-2001 Lees (BOST-) BOSTON HEART FOUND INC ₩, Lees RS, (first entry) Law 78 SW, ВP Arjona AA;

New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.

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Best Local Si
Query Match:
DB:
RESULT 2
AAV32838
ID AAV3
AC AAV3
XX O9-N
XX Huma
XX FT CDS
FT misc
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PR 26-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
 27-NOV-1996;
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 96US-0031930P
                         97WO-US021857
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67. .99
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RESULT 3
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA clone codes for novel human low density lipoprotein (LDL) binding protein LBP-2 (see AAW49041). It was isolated by screening human liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA clones (see AAV4834-39) and encoded rabbit and human LBPs (see AAW49037-42) are claimed. An abnormality in LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerotic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and vaccine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, useful for treatment and diagnosis of atherosclerosis and for identifying
                                                                                                     Ното
                                                                                                                                 .88
                                                                                                                                               atherosclerosis;
                                                                                                                                                                                                                                                                   AAH26494 standard; cDNA; 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1208
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                                                                                                                                            Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                    Human low
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WO200164874-A2

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Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; antiommune disorder; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds.
                                                                                                                                                   Human breast and ovarian cancer associated antigen gene SEQ ID 247.
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2000US-00616289.
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RESULT 5 AAH26499

AAH26499

DNA; 1614

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Pred. No.:
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                                                                                                                                                                                            Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antivical; antiallergic; hepatotropic; antibacteric; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist
                                                                                                                                                                                                                                                                                          Sequence 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatmen and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                           infectious diseases
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P-PSDB; AAB58957.
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treatment
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Human low density lipoprotein binding protein 2 (LBP-2) gene

12-NOV-2001 (first entry)

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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14-JUL-2000; 2000US-00616289.
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               AAH26495;
                                          AAH26495 standard; DNA; 12425 BP
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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAH26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of expression vectors, cells and methods of producing the LBPs. Methods for catlanting an agent for use in treating atherosclerosis, methods for treating a cell having an abnormality in structure or metabolism of LBP are claimed. Pharmaceutical compositions comprising an LBP polypeptide or metabolism of LBP are claimed. Pharmaceutical compositions comprising an labe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
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14-JUL-2000; 2000US-00616289.
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nucleic acid,
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                        and vaccine compositions, are also claimed
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                            The present sequence is that of a polynucleotide encoding a fragment of novel low density lipoprotein binding proteins (LBPs) of the invention (see AAB82797-820). LBPs are capable of binding to native and methylated low density lipoproteins (LDLs). Isolated polynucleotides encoding novel LBPs and their fragments are claimed, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000; 2000US-00517849.
14-JUL-2000; 2000US-00616289.
                                                                                                Sequence 84 BP;
                                                                                                                                                                                                                                                                                           New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.
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FH CDS
FT CDS
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                                             The present sequence is that of cDNA encoding a portion (see AAB82799) of CC novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA CC was isolated following screening of a rabbit cDNA library for clones CC encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The CC invention provides claimed polymucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated CC polypeptides, termed LBPs, and biologically active fragments and CC analogues of them, as well as expression vectors, cells and methods of CC producing the LBPs. Also claimed are methods of determining if an animal CC is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine CC compositions, are also claimed
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14-JUL-2000;
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Alignment Scores: Pred. No.: Score:

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Best Local Similarity:
Query Match:
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               The present sequence is that of cDNA encoding a portion (see AAB82800) of covel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA covel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA cover sisolated following screening of a rabbit cDNA library for clones conclude the cover state of the cover state 
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14-JUL-2000; 2000US-00616289.
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76.84%
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AAV32835
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                                       Lees AM,
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Alignment Scores: Pred. No.:
                                                                Sequence 1422 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;
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Percent Similarity:
Best Local Similarity:
       9.32e-06
104.50
96.30%
74.07%
76.84%
         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  1422
20
6
0
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US-09-976-740-20 (1-26) x AAH26490
GluGluGluGluhsphsphspgluhspGluhsphsp---ValSerGluGly
                                                           (1-1422)
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19

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TCGGAGGTGCCCGAGAGCGAT SerGluValProGluSerAsp 26 201

AAV32835 standard; cDNA; 1617 ВP

Rabbit low density lipoprotein binding protein LBP-2 CDNA

(first entry)

Low density lipoprotein binding protein; LDL binding protein 2; receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine; LBP-2;

Oryctolagus cuniculus.

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misc_feature
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                                     27-NOV-1996;
03-JUN-1997;
                                                                  26-NOV-1997;
                                                                                      04-JUN-1998.
                                                                                                       WO9823282-A1
                                                                                                                                             misc_feature
                                                                                                                                                                                                      misc_feature
                  (BOST-) BOSTON
Lees
RS,
                  HEART FOUND INC
                                     96US-0031930P.
97US-0048547P.
                                                                   97WO-US021857
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156. .1617
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/note= "Claim 20"
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                                                                                                                                                                                                                'note= "Claim 19"
                                                                                                                                                                                                                                             note= "Claim 5"
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note= "Claim 5"
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 Law SW,
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                                                                                                                                               . 660
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                                                                                                                             "Claim
Arjona AA;
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RESULT 11
AAH26488
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA clone codes for novel rabbit low density lipoprotein (LDL) CC binding protein LBP-2 (see AAM49038). It was isolated by functional screening of a cDNA library, produced from balloon-deendothelialised CC bealing rabbit abdominal aorta mRNA, for clones encoding LBPs able to bind both native and methyl LDL cDNA clones (see AAV32834-39) and cc encoded rabbit and human LBPs (see AAW49037-42) are claimed. An occ abnormality in an aspect of LBP metabolism or structure is diagnostic of a risk for atherosclerosis. The invention provides: methods for content and in a limit is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent formation of atherosclerosclerosic plaque; and methods for treating a cell having an abnormality in LBP structure or metabolism. Pharmaceutical and concine compositions are also provided, as well as recombinant vectors and host cells used to produce recombinant LBP
                                                                                                                                                                                                                                                                12-NOV-2001
                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                           Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                         AAH26488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding, treatment and diagnosis of atherosclerosis and for identifying
                                     WO200164874-A2
                                                                                                                                                                                                                                                                                                                   AAH26488 standard; cDNA; 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 11; 47pp; English.
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P-PSDB; AAW49038.
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                                                                                                                                                                                                                                                             (first entry)
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                                                               /partial
/note= "includes in-frame stop codon at nucleotides
28. .30"
                                                                                                                              Location/Qualifiers
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104.50
96.30%
74.07%
76.84%
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Matches:
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07-SEP-2001

Location/Qualifiers 246. .1928

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RESULT 12
AAH26500
ID AAH2
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of cDNA encoding a portion (see AAB82798) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit CDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical
Oryctolagus cuniculus.
                                                                                                       Rabbit low
                                                  Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis
                                                                                                                                         12-NOV-2001
                                                                                                                                                                               AAH26500;
                                                                                                                                                                                                               AAH26500 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated low density lipoprotein binding polypeptide for treating diagnosing and/or identifying therapeutic agents for atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
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14-JUL-2000; 2000US-00616289
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                                                                                                                                                                                                                                                                                       376
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                                                                                                                                                                                                                                                                                                                                                                            1 GluGluGluAspAspAspAluAspGluAspGluGluAspAsp---ValSerGluGly 19
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                                                                                                    density lipoprotein binding protein 2 (LBP-2) cDNA.
                                                                                                                                           (first entry)
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104.50
96.30%
74.07%
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Matches:
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                                                    therapy; diagnosis;
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20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4400
                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                         375
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RESULT 13
ACH46971
ID ACH46
XX
ACH46971
AC ACH46
XX
TO Alignment Pred. No.: Score: Percent Similarity:
Best Local Similarity:
Query Match:
DB: 밁 S 밁 Ş US-09-976-740-20 (1-26) The present sequence is that of cDNA encoding novel rabbit low density lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. The invention provides claimed polynuclectides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine WPI; 02-MAR-2000; 14-JUL-2000; Claim New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis. 28-FEB-2001; 07-SEP-2001 Sequence 2561 BP; 372 A; 937 C; 879 compositions, are also claimed Lees WO200164874-A2 genome Human 13-OCT-2003 US2003073623-A1 Homo sapiens ACH46971 No.: (BOST-) 1320 1260 2001-565505/63 DB; AAB82807. AM, 4; Fig infant 20 ss; sequencing mapping; biodiv μ BOSTON HEART standard; cDNA; 415 SerGluValProGluSerAsp TCGGAGGTGCCCGAGAGCGAT Lees RS, 2000US-00517849 2000US-00616289 2001WO-US006356 2A; 143pp; English brain cDNA #1034. (first entry) biodiversity; genetic disorder 1.73e-05 104.50 96.30% 74.07% 76.84% x AAH26500 Law FOUND INC by hybridisation; SBH; expressed ws, Arjona 먥. (1-2561)1340 26 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: AA; G; 373 T; 0 2561 0 1 U; 0 Other; sequence tag; 19 밁

New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein, WPI; (LABA/) (STAC/) (DICK/) 30-JUL-2001; 2001US-00918995 30-JUL-2001; 2001US-00918995 17-APR-2003. (JONE/) 2003-615964/58. STACHE-CRAIN DICKSON M C. JONES L W. RT, DRMANAC R T. LABAT Labat I, W Stache-Crain 'n Dickson М С cDNA libraries, useful chromosome and gene Jones Ę

Claim 1; SEQ ID NO 34183; 44pp; English.

antisense DNA or RNA.

or in generating

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACHI-2789-ACH50831, whose sequence was CC determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypeptide comprising a sequence corresponding to CC a reading frame of the novel polynucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (EST) for clantifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide corrections are also useful as hybridisation probes, as oligomers for PCR, CC protein, or in generating antisense NNA or RNA. The purified polypeptide is useful for generating antisense NNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence correction of this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623

Sequence 415 вÞ; 97 A; 92 C; 146 <u>ი</u> 80 T; 0 ₽, 0 Other;

Query Match: DB: Best Score: Percent Similarity: Pred. No.: Alignment Scores: Local Similarity: 0.000577 88.00 86.96% 60.87% 64.71% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 

US-09-976-740-20 (1-26)x ACH46971 (1-415)

Ş á 밁 163 21 **--**GluValPro GACGATGAGGAAGAGGATGAAGATGAAGACGACGATGATGATGAGGAGGATGGTGAT 222 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 23 20

RESULT 14 ACH12859

223

GAGGTGCCT

231

ACH12859 standard; cDNA; 421 BP

ACH12859;

13-OCT-2003 (first entry)

Human adult brain CDNA #71.

genome Human; ss; sequencing by hybridisation; SBH; expressed mapping; biodiversity; genetic disorder. sequence tag; EST;

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AAQ34771
ID AAQ
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                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide comprising any one of CC 38043 cDNA sequences, appearing as ACHI-2789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also CC included is a purified polypaptide comprising a sequence corresponding to CC a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for equences in forensics, in assessing biodiversities, or in identifying mutations CC in forensics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                      Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences obtained i
as hybridization probes, as oligomers i
mapping, in the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LABA/)
(STAC/)
(DICK/)
(JONE/)
                                                                                                                                                                                                                                                                                                                                                                         Sequence 421
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                                                       AAQ34771
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06-MAY-1993

(first entry)

Search completed: March 12, Job time: 47.2118 secs

2004, 21:08:35

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                                                                                                                                         Percent Similarity:
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                                                                                                                   : Local S
ry Match:
                                                                                                                                                                                                                Total RNA was extracted from Jurkat cells and mRNA was prepd. from it. A CDNA library was prepd. in lambda gtll. A positive clone was isolated and analysed by antibody screening. A mutant coding sequence in which the 3'-terminal sequence was deleted was prepd. and used to prepare a polypeptide in which the C-terminal end is deleted. Epitopes of the CENP-B protein were determined. These peptides can be used to detect antihuman centromere antibodies. The type of diseases of a patient having the antibody can be exactly classified using the polypeptide
                                                                                                                                                                                              Sequence 489
                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                         and identification of
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GAGGTGCCT
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-MODEL=frame+ p2n.model p-DEV=xlp
-MODEL=frame+ p2n.model p-DEV=xlp
-Q=/Ggn2 1/USPTO_spool p/US09976740/runat 10032004 094549 19564/app_query.fasta_1.1898
-Q=/Ggn2 1/USPTO_spool p/US09976740/runat 10032004 094549 19564/app_query.fasta_1.1898
-DB=Issued PatenEs_NA -QFMT=fastap -SUFFIX=rni -MINWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -ND=-1 -MARIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -ND=-1 -MRX=100 -THR MIN=0 -ALIGN=15
-LIST=45 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTSMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-MODE=LOCAL -OUTSMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09976740 @CGN 1 1 235 @runat 10032004 094549 19564 -NOPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG-SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=10 -WARN TIMEOUT=30 -FIREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=10 -VARN TIMEOUT=30 -FIREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=10 -VARN TIMEOUT=30 -FIREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                  Query
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-979-608A-31

US-09-517-849-31

US-09-616-289-31

US-08-979-608A-16

US-09-517-849-16

US-09-616-289-46

US-09-616-289-50

US-09-616-289-50

US-09-616-289-50

US-09-517-849-37

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Sequence 16.
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Sequence 45.
Sequence 45.
Sequence 37.
Sequence 37.
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GENERAL INFORMATION:
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equence 27, App equence 27, App		equence 22, App	equence 1, Appl	equence 1, Appl	equence 1, Appl	equence 3, Appl	nce 3, Appl	equence 3, Appl	equence 3, Appl	equence 20, App	equence 20, App	equence 20, App	equence 1, Appl	equence 1, Appl	equence 1, Appl	equence 10, App	equence 10, App	equence 30, App	equence 30, App	equence 30, App	equence 3, Appl	equence 48, App	equence 11, App	equence 11, App	equence 11, App	equence 13, App	equence 13, App	equence 13, App	ence 12, App	equence 12, App

## ALIGNMENTS

APPLICANT: Lees, Ann M.

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COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NO. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORES LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 Franklin
                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arjona, Anibal A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lees, Robert
Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREATING ATHEROSCLEROSIS
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-517-849-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application Patent No. 6605588
GENERAL INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: PASICSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATIONA, ANIDAI A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPRONE: 617/542-5070
TELEPRAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lees,
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STATE: MA
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                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09517849
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APPLICANT: Lees, ROBERT S.
APPLICANT: Lew, SIMON W.
APPLICANT: Law, SIMON W.
APPLICANT: APIONA, ANIDAI A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US/09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/979,608
PRIOR FILING DATE: 1900-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION DATE: 1997-06-03
                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78
TYPE: DNA
CRGANISM: Homo sapiens
US-09-616-289-31
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Best Local Similarity:
Query Match:
                                           US-09-976-740-20 (1-26) x US-09-616-289-31 (1-78)
                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-976-740-20 (1-26) x US-09-517-849-31 (1-78)
                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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No. 6632923
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GluGluGluGluAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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Matches:
Conservative:
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Indels:
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Matches:
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US-08-979-608A-16
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                                                                                                                                                                                                        Percent Similarity:
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GENERAL INFORMATION:
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                                                                                                                                                                                       Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION UNMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 03-JUN-1996
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REFERENCE/DOCKET NUMBER: 10797-002001 (forme:
TELEPHONE: 617/542-8906
NFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 1...651 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                   FEATURE
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                  21
                                                    22
GluValProGluSerAsp
                                                                       GluGluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110-2804
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
Query Match:
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US-09-517-849-16
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GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
82 GAAGTGCCCGAGAGTGAC
                             21 GluValProGluSerAsp 26
                                                               82 GAAGTGCCCGAGAGTGAC 99
                                                                                 1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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99
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Matches:
Conservative:
Mismatches:
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RESULT 6 US-09-616-289-16 ; Sequence 16, Application US/09616289

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APPLICANT: AJONA, ANIABAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; GRGANIEM: Homo sapiens; FEATURE; NAME/KEY: CDS; LOCATION: (1)...(651)
US-09-616-289-16
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/97,608
PRIOR APPLICATION NUMBER: US 60/91,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER: OF SEQ ID NOS: 53
NUMBER: FEATSO FOR WINDERS US 60/048,547
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US-09-616-289-45; Sequence 45; A;
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DB:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal
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; SOFTWARE: FastSEQ for Wil

SEQ ID NO 50

; LENGTH: 12425

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-616-289-50
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APPLICANT: ATJONA, ANIMAL A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR PRICATION NUMBER: US 68/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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; LOCATION: (1)...(1614)
US-09-616-289-45
                                                                       US-09-976-740-20 (1-26) x US-09-616-289-50 (1-12425)
                                                                                                                                                                                           Score:
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                                                                                                                                Query Match:
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SEQ ID NO 45
LENGTH: 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
1045 GAAGTGCCCGAGAGTGAC 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50, App.
o. 66329:
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                      GluGluGluGluAspAspAspGluAspGluAspGluGluAspAspValSerGluGlySer
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Law, Simon W.
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136.00
100.00%
100.00%
100.00%
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100.00%
100.00%
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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COMPUTER: IBY COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/99,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UNN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-979-608A-37
; Sequence 37, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
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                                                                                                                                   US-09-976-740-20 (1-26) x US-08-979-608A-37 (1-84)
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arjons, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
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                     SerGluValProGluSerAsp 26
                                                                    GluGluGluAspAspAspGluAspGluAspGluGluAspAsp---ValSerGluGly 19
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
   TCGGAGGTGCCCGAGAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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Law, Simon W
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104.50
96.30%
74.07%
76.84%
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   84
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 11
US-09-616-289-37
; Sequence 37, Application US/09616289
; Patent No. 6632923
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RESULT 10
US-09-517-849-37
; Sequence 37, Application US/0951
; Patent No. 6605588
; Patent No. 6605588
; GENERAL INFORMATION: Lees, Ann M.
; APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                            US-09-976-740-20 (1-26) x US-09-517-849-37 (1-84)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 1079
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5976
TELEPHONE: 617/542-5976
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
64 TCGGAGGTGCCCGAGAGCGAT
                               20 SerGluValProGluSerAsp 26
                                                                                             1 GluGluGluAspAspAspGluAspGluAspGluGluAspAsp---ValSerGluGly 19
                                                                         LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence LOCATION: 1...84
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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Arjona, Anibal A.
OF INVENTION: NOVEL LO
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104.50
96.30%
74.07%
76.84%
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                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 37:
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10797-003001
                                                                                                                                                                                                      Mismatches:
Indels:
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Conservative:
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PRIOR APPLICATION DATA:

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APPLICANT: Arjona, Anibal A.

APPLICANT: Arjona, Anibal A.

ITITLE OF INVENTION: NOVEL LOW DENGITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: AFHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Aniba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 84
TYPE: DNA
ORGANISM: Homo sapiens
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                            TREATING ATHEROSCLEROSIS NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 TCGGAGGTGCCCGAGAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                                                                            STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08979608A
                                                                                                                                                                                                                                                                                                                                                   Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                             Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert S.
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74.07%
76.84%
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Robert S.
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Matches:
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Indels:
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RESULT 13
US-09-517-849-12
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Best Local Similarity:
Query Match:
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LOCATION: 1...696;
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-979-608A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
TYPE: nucleic acid
STRANDENESS: single
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-UTW-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GluGluGluAspAspAspAspGluAspGluAspGluGluAspAsp---ValSerGluGly 19
                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lees, Ann M.
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104.50
96.30%
74.07%
76.84%
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Matches:
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ATTORNEY/AGENT INFORMATION:

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APPLICANT: Lees, ....
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-66-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
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US-09-616-289-12
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DB:
    Alignment Scores: Pred. No.:
                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(696)
US-09-616-289-12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
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LENGTH: 1362 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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Indels:
Gaps:
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Matches:
Conservative:
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US-08-979-608A-13
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Percent Similarity:
Best Local Similarity:
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Best Local Similari
                                                  Pred. No.:
                                                                  Alignment Scores:
                                                                                                     US-08-979-608A-13
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GENERAL INFORMATION:
                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
TYPE: nucleic acid
STRANDEDURSS; single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION UNMSER: US/08/979,608A

FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION NUMSER: US 60/048,547

FILING DATE: 03-UN-1997

APPLICATION NUMSER: US 60/048,547

FILING DATE: 03-UN-1997

APPLICATION NUMSER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Wyers, Louis

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 617/542-5070
                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lees, Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GluGluGluGluAspAspAspGluAspGluAspGluGluAspAsp---ValSerGluGly 19
                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAW, SAME AND LAWSITY LIPOPROTEIN
OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
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Law, Simon W
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                Length:
Matches:
Conservative:
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Conservative:
Mismatches:
Indels:
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   Mismatches:
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